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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: September 14, 2004, 15:03:35 ; Search time 13362 Seconds (without alignments) 6967.582 Million cell updates/sec
Title: US-09-813-329-5 Perfect score: 2148 Sequence: 1 ggcacgaggggaacggacgtaaaaaaaaaaaaactcgag 2148
Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database : GenEmbl:* 1
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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LEGIVVALIALTIWQTTRVSHILDKELKSLKRVVDNLQQRLGINYLDFDEFQREYEN
ALI DYPKKVDGLTDEEDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLN
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SHDQNGFI TYCGQTPFLOCLNTVPTNMPHKVHTCHTSGLIHLBRNBERIHLKDIHNDRN
AVLREGNNRSYPGIFKV"
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George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S. Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
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Lawrence Berkeley National Laboratory, of Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
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/product="RH51659p"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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Location/Qualifiers
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Direct Submission
Submitted (10-MAY-1999) Department of Pathology, Comprehensive
Cancer Center, 1500 E. Medical Center Dr., Ann Arbor, MI 48109,
Location/Qualifiers
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae; Drosophila.

[ bases 1 to 2101)
Inohara,N. and Nunez,G.
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Inohara, N. and Nunez, G.
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	TOTGAGGTTGTTCTGTGCTCGTAGTATCTTAAAATACATGCTTATCTTCATCTGTCATCTTCATCTGTGTTCTTCATCTGTAGAGGTTGTTCTGTTGTAGTACTTAAATACATAGTTGTTCTTTAAATACATAGTTCTTCTTGTTAGTAGTTAGT	SP GS	1487 AAGGAAGTATGGGCTACCATGGAGATATGTACATAGGAAATGATAACGAGAGAACTCTT 1546
	GTGCGACAAAGCTCGATTGGAAACAGCTGTCGAGTGCCCTTTGAGTGGGCGAGAAGTCG 5	S S	1547 ATCAGGGACACTTTCAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATT 1606
	TCATCATCATCATCGTCGTTATCAACAGAATCAGCATCAGCATCTGGAGGCCCCGGT 6	දු දු	1607 ACGTATACGCCCAGATATGCTACAACAACTCGCACGACAACGGATTTATCGTCTTTC 1666
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="eiger"
427. .1656
/gene="eiger"
codon_start=1
/evidence=experimental
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ALIDYPKKVDGLTDEEDDDDGGDGLDSIAADDEDDDVSYSSVDDVGADYEDYEDFGKEYEN
ALIDYPKKVDGLTDEEDDDGGGLDSIAADDEDDVSYSSVDDVGADYEDYEDFGKEYEN
ALIGYRTRFLQREKSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSRRRHQSNAGTHGMYTOMTSYRGETDSASSASNDDWNFDDFTSYNAHKKVGEKKSRSTADVRN
BEGNIAGNTRFLQREKSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSRRRHGSNAGTHGMYTOMTSYRGETTYPTNMPHKVHTCHTSGLIHLBRNERIHLKDIHNDRN
AVLREGNNRSYFGIFKV"
                                                                                   1656 bp mRNA linear INV 27-JUN-2002 mRNA for TNF superfamily ligand, Eiger,
                                                                                                                                                                                                                                                                                        Jaki,T.

Jaki,T.

Direct Submission

Direct Submission

Experiment (02-NOV-2001) Tatsushi Igaki, Brain Science Institute,

RIKEN, Laboratory for Cell Recovery Mechanisms; 2-1 Hirosawa, Wako,

Saitama 351-0198, Japan (E-mail:igaki@brain.riken.go.jp,

Tel:81-48-467-6945, Fax:81-48-467-6946)
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Aigaki,T. and Miura,M.
Eiger, a TNF superfamily ligand that triggers the Drosophila
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/dol_trace="taxon:7227"
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100.0%; Pred. No. 0;
iive 0; Mismatches
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EMBO J. 21 (12), 3009-3018 (2002)
                                                                                           Drosophila melanogaster
complete cds.
AB073865
AB073865.1 GI:21623741
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OICYNNSHDONGFIVFQCDTPFLQCINTVPTNMPHKVHTCHTSGLIHLERNERIHLKD
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                                                                                                                                                                                                                            extracellular domain"
                                                                                                                                                                              domain"
                                                                                                                               'note="Region: intracellular domain'
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Pred. No. 1.6e-263;
); Mismatches 0;
                                                                                                                                                                              transmembrane
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/gene="darth"
/note="cleavage site"
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/gene="darth"
/note="Region: t
178. .1245
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/note="Region:
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Best Local Similarity 98.6
Matches 1230; Conservative
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| IGLGLVVAILALTIWQTTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases I to 1248)
Kaupplla,S., Maety,W.S., Chen,P., Tomar,R.S., Eby,M.T., Chapo,J.,
GATAACGAGAGAAACTCTTATCAGGGACACTTTCAAACGCGGGATGGCGTCTTGACGGTG
                                                                                                                                 ACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACAACAACAACAGCAGACAG
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                                                                                                              ACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACAACAACTCGCACGACCAG
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Eiger and its receptor, Wengen, comprise a TNF-like system
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
/map="2R"
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Center, 5323 Harry Hines Blvd., Dallas, TX
Location/Qualifiers
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/gene="darth"
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/gene="darth"
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Chaudhary, P.M.
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1513 ATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTTCAAACGCGGGAT 1572
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                                                                                                             melanogaster"
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170. .955
                                                                                                          /organism="Drosophila
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Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
Science 2000). The sequence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accuracly this particular cDNA clone, However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAS, and
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AGCCAGATCCGAGGACTCGAGGCCAGCAGCC
                                                                 CTAGTCCGCAAAGGTGAATCTCTTTCAGCCAGATCCGAGGACTCGAGGCCAGCAGCC
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170. . 955 170. . 955 /gene="CG12919" /note="Longest ORF" /codon start=1 /product="SD18286p" /product="AAM51093.1" /db_xref="G1:21430930" /db_xref="G1:21430930" /db_xref="E1YBASE:FB90033483" /db_xref="FLYBASE:FB9001GOWHFELQEKSSASANDDNVFDDFTS
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HRHJLVRKGESILLGARSEDSFRAAHFHLSSRRRHGGSMGYHGDMYIGNDVENDFTS
FQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQCLNTVPTNNFHKVH
TCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV" reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to constitutily.berkeley.edu. 1110 2 1050 1170 1290 GAGCAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACT 1350 TCCAAAGAGGCCCTGCACCACTTCACCACCGTCGCAGAATGCATTCCCGGCCATCGCCAC 1410 1512 1452 990 124 184 244 364 424 544 64 931 TACGAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGAC GACGACGATGGCGATGGTTTCCATTGCGGACGACGACGACGACGACGTTAGCTAT AGCICTGTGGATGATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATTAAACTC 125 AGCTCTGTGGATGTTGGCGCAGACTACGAGGACTACACCCGATATGTTAATAAACTC 1111 AACAATGCACATACCGGCACCACGCCCACTGTGAGACCACTGCTGAGGGCGAGGGCGAG 1171 ACGGACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTCGATGACTTTACCAGGTAC AATGCCCACAAAAAGAAGCAGGAGAGAAATCTCGCTCGATTGCCGATGTACGCAATGAG 65 GACGACGATGGCGATGGTCTGGATTCCATTGCGGACGACGACGACGACGACGACGACGTTAGCTAT 6 TACGAGAATGCCCTCATCGACTATCC-CAAAAGGTGGATGGCCTCACGGATGAGGAGCAC 365 GAGCAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACT GCCCATTTCCACCTGAGCAGCAGCGGCGTCACCAAGGAAGTATGGGCTACCATGGAGAT Gaps -----AGCCAGATCCGAGGACTCGAGGCCAGCA GCCCATTTCCACTTGAGCAGCAGGGGGGTCACCAAGGAAGTATGGGCTACCATGGAGAT 19; Length 1221;

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Drosophila melanogaster (fruit fly)
                             Score 798.8; DB 2;
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, *** SEQUENCING IN PROGRESS ***.
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GGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACAAC
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                                          GGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACAAC
                                                                                                 AACTCGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCATTCCTGCAGTGC
                                                                                                               TTGAACACGGTGCCCACCAACATGCCACATAAGGTGCACACCTGCCACACGAGTGGTCTG
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HTG; HTGS PHASE2.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Adams,M. and Venter,J.C.
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For further information on this sequence you may e-mail
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This sequence will be replaced
by the finished sequence as soon as it is
the accession number will be preserved.
Location/Qualifiers
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Submitted (03-NOV-1999) Celera Genomics, 45
Rockville, MD, USA
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Endopterygota; Dispera; Brachycera; Muscomorpha; Bebydroidea; Drosophila.

1 (bases 1 to 158983)

Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhofff,C., Champe,M., Chaez,C., Chew,M., Clesiolka,L., Doyle,C.M., Farfan,D.E., Chew,M., Clesiolka,L., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kin,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Feiffer,B., Poon,L., Punch,E., Sedusira,A., Sethi,H., Snir,E., Svirskas,R.R., Twomery,B., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M. Sequencing of Drosophila chromosome 2R, region 46E1-46F6

Lupublished (1998)

2 (bases 1 to 158983)

Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Rarra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Fefifer,B., Poon,L., Punch,E., Pacleb,J.M., Park,S., Felifer,B., Poon,L., Punch,E., Sethi,H., Snir,E., Sieran,L.L. and Rubin,G.M.

Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.

Submitted (19-NoV-1988) Berkeley Drosophila Genome Project, MS Berkeley, CA 94720, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Pl library locations: 53-41, 20-89, 54-93.
Location/Qualifiers
1. 158883.
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/note="These Pls were completed as a project. DS05181
[D384] is a partial bridge with list distal neighbor
extending from pl to pl end at bp 57,624. DS01913 (D350)
extends from Pl end at 7,924 to pl end at 92,484. DS05033
(D347) extends from Pl end at bp 80,881 to Pl end at bp
158,983. Between bps 53,139 and 53,140, Th10 was excised
from DS05181 along with an associated 9 bp duplication."
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/clone="Pls DS05033 (D347), DS01913 (D350), and DS05181
(D384)"
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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/mol_type="genomic DNA"
/strain="Y2; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
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Best Local Similarity 99.8
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Lobophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilade; Drosophila.

S Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Besson, K.Y., Busam, D.A.,

Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Garg, N.S., George, R.A.,

Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,

Gonzalez, M. Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoc, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Scheeler, F.,

Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
134476 direreritiririritiririririceriricecrerecerriareecaaacaaaacidar 134417
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AC007414.6 GI:15451491
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us-09-813-329-5.rge

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Unpublished

2 (bases 1 to 189620)

8 Calniker, S., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
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Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., May, M., Wurphy, B., Walson, K.A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Parel, S., Pfeiffer, B.,
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Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
Direct Submission

AL Submitted (08-NOV-2001) Berkeley Drosophila Genome Project, MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ephydroidea, Drosophilidae; Drosophila, Brach, Celaiker, S. B., Adams, D., Kronmiller, B., Tyler, D., Wan, K.H., B. Celaiker, S. B., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Bardwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J. W., Center, A., Champe, M., Davenport, L.B., Dietz, S. M., Dodson, J. W., Frise, E. Galle, R. F., Gargi, N.S., George, R. A., Frise, E. Galle, R. F., Gargi, N.S., George, R. A., Houck, J., Hoskins, R.A., Hostin, D., Howland, T. J., Inseyam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntcosh, T. C., Moy, M., Wurphy, B., Nelson, C., Nelson, K.A., Nunco, J., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S. M., Zaveri, J.S., Smith, H.O., Rubin, G. M. and Venter, J. C. Sequencing, of Drosophila chromosome 2R, region 46D-47A
                                                                                                                                                                                                                                                                                                                                                                                                                                 133826 TGCTCTAAGATCCCCCGGTGTTCATCAATTATGACTGCCGAGACCCTCAAGCCGTTTATAA 133885
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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L Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
ON Sep 6, 2001 this sequence version replaced gi:13324748.

Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133346 ATTGAATTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACTGTGT 133405
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/clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
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Sequencing of Drosophila chromosome 2R, region 46C-46D
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ABELDHGKRI ISAASDGLLKLWNIKTNTCLQSLDBENDRWANLAVSARSNRFFYTGGA
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Pred. No. 9.3e-171;
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Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwan, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M., Sequencing of Drosophila melanogaster genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JAN-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA On Jul 1, 2002 this sequence version replaced gi:10727672.
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WQLDTGKLVKLWKAQHKGPVIRVEFSPCGRLICTSGGADATLRLWDYSNNSCLGALKD
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                                                                                                                                                                                                                                                                                                                                                                                                                              Misra, S., Crosby, M.A., Matthews, B.B., Bayraktaroglu, L.,
Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochnik, S.E.,
Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W.,
Celniker, S.B., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., de
Grey, A.D.N.J., Harris, N.L., Kronmiller, B., Marshall, B.,
Milburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E.,
Shu, S., Smutniak, F., Whitfield, E.J., Ashburner, M., Gelbart, W.M.,
Rubin, G.M., Mungall, C.J. and Lewis, S.E.
Annotation of Drosophila melanogaster genome
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Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
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'note="last curated on Mon Peb 11 17:53:43 PST 2002"
'map="46B7-46B9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
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mol type="genomic DNA"
db_xref="taxon" 7227"
chromosome="2R"
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join(197. .286,346. .2954)
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join[281. .286,346. .2683)
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         Yamada, S.
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                                                                                                                        Takeuchi, K., Yamashita, S. and Yamada, S.
Takeuchi, K., Yamashita, S. and Yamada, S.
Direct Submission
Submitted (14-MG-2003) Kazuharu Takeuchi, Nippon Suisan Kaisha,
Ltd., Central Research Laboratory; Kitanomachi, Hachioji, Tokyo
192-0906, Japan (E-mail:k-takeuchi@nissui.co.jp,
Tel:81-426-56-5195, Fax:81-426-56-5188)
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                   and Yamashita,S.
Aspolin, a Novel Extremely Aspartic Acid-rich Protein in Fish
Muscle, Promotes Iron-mediated Demethylation of
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      Kimura, M., Seki, N., Kimura, I.,
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ilarity 50.6%; Pred. No. 0.00031;
Conservative 0; Mismatches 158; Indels 0.
                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/frissue_type="skeletal muscle"
/country="Japan: Hokkaido, Hakodate"
                                                              Trimethylamine-N-oxide
J. Biol. Chem. 278 (48), 47416-47422 (2003)
22995865
                                                                                                                                                                                                                                                                 organism="Theragra chalcogramma"
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    Takeuchi, K., Hatanaka, A.,
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/gene="aspolin2"
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mRNA for aspartic acid-rich protein
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Theragra chalcogramma
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra;
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                                                 AAAACTAGAAAATATCTTGAGAAACTTGTTTTCGCGCTTTTTCTTTTGCTAATTGCCGATC
                              CGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTAACAAG
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Gold,L., Tuerk,C., Pribnow,D. and Smith,J.Drew.
Systematic polypeptide evolution by reverse translation
Patent: US 6194550-A 7 27-PEB-2001;
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Pred. No. 0.00024;
0; Mismatches 187; Indels
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/mol_type="unassigned DNA"
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Sequence 7 from patent US 6194550.
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AR135147.1 GI:14124052
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Similarity 48.9%;
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                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii; Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Paracanthopterygii, Gadiformes, Gadidae, Theragra.
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                                                                                                                                                                                                                                                                 Takeuchi, K., Hatanaka, A., Kimura, M., Seki, N., Kimura, I., Yamada, S. and Yamashita, S. Aspolin, a Novel Extremely Aspartic Acid-rich Protein in Fish Muscle, Promotes Iron-mediated Demethylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-AUG-2003) Kazuharu Takeuchi, Nippon Suisan Kaisha, Submitted (14-AUG-2003) Kazuharu Takeuchi, Nippon Suisan Kaisha, Ltd., Central Research Laboratory, Kitanomachi, Hachioji, Tokyo 192-0906, Japan (E-mail:**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561 ATGATGATGACGACGACGATGATGATGATGACGATGACGACGACGACGATGACGATG
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1. .2235
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J. Biol. Chem. 278 (48), 47416-47422 (2003)
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/db_xref="taxon:48550"
/tissue_type="skeletal muscle"
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Takeuchi, K., Yamashita, S. and Yamada, S.
Direct Submission
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Theragra chalcogramma (Alaska pollock)
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Patent: WO 03000898-A 5263 03-JAN-2003;

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/organism="Oryza sativa"
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder; sparse hair; sweat gland aberration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; TNFv2; obesity-linked insulin resistance; gene; ds.
                                                                                                                                                                                                                                                             /note= "Tumour necrosis factor variant 1" 634. .1860
                                                                                                                                                                                                                                                                                  /*tag= d
/note= "Specifically claimed in claim 22"
634. 789
                                                                    encoding tumour necrosis factor variant 2 (TNFv2)
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/label= mature_TNFv1
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634. .1863
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product= "TNFv1"
BP.
ABK11680 standard; DNA; 2148
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                                                                                                                                                                                       Drosophila melanogaster.
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(CHEN/) CHEN J.
(RAMA/) RAMANATHAN C S.
(XIAO/) XIAO H.
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Human

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us-09-813-329-5.rng

New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals. Claim 2; Fig 3A-C; 119pp; English Ramanathan PM, Chen J, 2002-195121/25 GUAN B. BOWEN M A. P-PSDB; AAU77718 Carroll (GUAN/) (BOWE/)

controlling

Bowen MA

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The invention describes an isolated tumour necrosis factor polypeptide (TMF). The polypeptide and polymucleotide are useful in controlling agriculturally important peers, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polymucleotide are useful for modulating the polypeptide and polymucleotide may be useful for modulating the polypeptide and polymucleotide may be useful for treating. Thus anelorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), chotoxic shock, inflammation, haemorrhagic necrosis of tumours, cyctoxicity and obesity-linked insulin resistance, all of which involve consists factor variant 2 (TNFv2) protein, described in the invention

Sequence 2148 BP; 645 A; 510 C; 506 G; 487 T; 0 U; 0 Other;

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ö 120 120 180 180 240 300 9 9 240 TGATAAAACTAGAAAATATCTTGAGAAACTTGTTTTCGGGGCTTTTTTGCTAATTGCC 300 GATCGCGGAAGAGAAAAAAGAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAG 360 360 420 420 480 480 540 540 GGCACGAGGCGAACGTTTAAAGTGAGAAAAGAAACCGGTAAATCAGAGATCCCAAG CAAGATTGAATTTCGCCATCGGCAAATTACTAAAATACATAAGTGCAACTCGTCCACT GTGTGTTGTGTTTTTTTTTTTTTTTGGTTTTGGCTGTGCCTTTATCGCAAAGAACAAGAAC GGCACCATCAGCAGCCCGAGGGGTTTATCTATAGATGTCGCAGCTTATCATCTCATGC TGTCTGTGAGGTTGTTCTGTGTGCTCGTGTAGTATCTTAAATACATAGAGTGTGTTCATA Gaps o, DB 6; Length 2148; Indels .; 0 Query Match
100.0%; Score 2148;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2148; Conservative 0; Mismatches 61 61 121 121 181 181 241 241 301 301 361 361 421 121 181 481

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1020 1080 1080 1260 009 99 1020 TCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCATCCTCAGGCTCAAATGAT 1200 99 720 720 780 780 840 1560 840 900 900 960 960 ATAIGCTACAACAACTCGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCA 1680 ATCGTCATCATCATCATCGTCGTCATTATCAACAGAATCAGCATCAGCATCTGGAGGCCC CGGTTGCTCTAAGATCCCCAGTGTTCATCAATTATGACTGCCGAGACCCTCAAGCCGTTT ATAACGCCAACGAGTGCCAACGATGATGATTTCCGGCCAAAGCGACCAGCACGACGACC ATAACGCCAACGAGTGCCAACGATGATGGTTTTCCGGCCAAAGCGACCAGCACGGCGACC GCCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTTTGGGGTTCATCGGTCTGGGGCTG GCCCAGCGACCCCCCCCCCCCCCCCCCCCGGTTTTGGGGTTCATCGGTCTGGGGCTG GTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGTGTATCGCATCTGGACAAG GAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTTGGGCCATAAACTAT CTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAA AAGGTGGATGGCCTCACGGATGAGGACGACGACGACGATGGCGATGGTCTGGATTCCATT GCGGACGACGACGACGACGTTAGCTCTGTGGATGATGTTGGCGCAGACTAC GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACCACA GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACGCCCACA 1141 TCTGAGACCACTGCTGAGGGCGAGGCGAGGCGGACGCGTGCATCCTCAGCCTCAAATGAT GACAATGTGTTCGATGACTTTACCAGCTACAATGCCCCACAAAAAGAAGCAGGAGAAAA GACAATGTGTTCGATGACTTTACCAGCTACAATGCCCACAAAAAGAAGGAGGAGAAAAAA CTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAGAGAGCCCTGCACCACTTCACCAC TCGAGGCCAGCAGCCCATTTCCACTTGAGCAGCAGGCGTCACCAAGGAAGTATGGGC TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATTTCAAGGAAATCACACAGAG CGTCGCAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGCCAGATCCGAGGAC CAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAG TACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTT CGGTTGCTCTAAGATCCCCAGTGTTCATCAATTATGACTGCCGAGACCCT 541 601 601 199 661 721 721 781 841 781 901 196 1021 1081 1081 1141 1201 1201 1261 1261 1321 1321 1381 1381 1441 1441 1501 1501 1561 1621 1561 qq ð g ò g à ď ò g ò g ò g 8 g Q ò 8 ద ò 셤 ò Db ò 임 ò g g ઠે ò g δ g ò ద à

Bowen MA;

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New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm
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RAMANATHAN C 8
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BOWEN M A.
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                                                                                                                     GATCGCAATGCAGTTCTGCGGGGGGGAAACAACGGAAGCTACTTTGGCATCTTCAAGGTG
                                                                   ACGAGTGGTCTGATCCACCTGGAACGAAACGAGGATCCATCTGAAGGACATTCACAAC
                                                                              ACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCATCTGAAGGACATTCACAAC
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652. .807
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652. .1881
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The invention describes an isolated tumour necrosis factor polypeptide and polynucleotide are useful in controlling agriculturally important pests, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating controlling modified and polynucleotide are useful for modulating the polypeptide and polynucleotide may be useful for treating. Thus controlling or preventing X-linked anhidrotic (hypohidrotic) ectodermal or sysplasia and X-linked anhidrotic (hypohidrotic) ectodermal or sweat like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), condotoxicity and obesity-linked insulin resistance, all of which involve TNF molecules. This sequence encodes the drosophila melanogaster tumour necrosis factor (TNF) protein, described in the invention
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Claim 2; Fig 1A-C; 119pp; English
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            TGTCTGTGAGGTTGTTCTGTGTGCTGTAGTATCTTAAATACATAGAGTGTGTTCATA
                                                                           ATCGTCATCATCATCGTCGTCATTATCAACAGAATCAGCATCAGCATCTGGAGGCCC
                                                                                        GCCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTTTGGGGTTTCATCGGTCTGGGGCTG
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                                           CGAGTGCCCTTGAGTGGGTGGGCAAG
                                                                                                                  CGGTTGCTCTAAGATCCCCAGTGTTCATCAATTATGACTGCCGAGACCCTCAAGCCGTTT
                                                                                                                                                       ATAACGCCAACGAGGCCAACGATGGTGTTTTCCGGCCAAAGCGACCAGCACGGCGACC
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                    GAGAATGCCCTCATCGACTATCCAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated tumour necrosis factor polypeptide (TNF). The polypeptide and polynucleotide are useful in controlling agriculturally important peets, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating captubalial morphogenesis, cell-matrix adhesion in files and mammals. Thus the polypeptide and polynucleotide may be useful for treating, ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), endotoxic shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obesity-linked insulin resistance, all of which involve TNF molecules. This sequence encodes the drosophila malanogaster tumour necrosis factor variant 1(TNFv1) protein, described in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals.
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RAMANATHAN C &
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Claim 1; SEQ ID NO 15889; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                               Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
           Drosophila melanogaster genomic polynucleotide SEQ ID NO 15892
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                                                                                                                                                                                                                                                                                                                                                                                                                                               42.2%; Score 907.4; DB 4; Length 978; 98.0%; Pred. No. 9.5e-196; ive 0; Mismatches 1; Indels 18
                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 15892; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 978 BP; 289 A; 261 C; 238 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                      Myers EW;
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                                                                                                                                               23-MAR-2000; 2000US-0191637P.
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Conservative
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genes from Drosophila and
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                                                              Drosophila melanogaster.
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                                                                                                      CACCTCCTAGTCCGCAAAGGTGAATCTCTTTCAGCCAGATCCGAGGACTCGAGGCC
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          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL01840-ABL1675) and the encoded proteins (ABBS7077-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                         Sequence 3324 BP; 918 A; 715 C; 681 G; 1010 T; 0 U; 0 Other;
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                                                                                                                      The sequence is that of an example randomising oligomucleotide which is used in the prepn. of mRNA encoding candidate polypeptides for the method of systematic polypeptide evolution by reverse translation (SPERT). The method provides a rapid way of isolating and identifying polypeptide ligands which bind to target mole. The polypeptide ligands can be used in e.g. assay methods, diagnostic procedures, cell sorting, as activators or inhibitors of target mol. function, as probes, as sequestering agents, drug delivery vehicles, modififers of hormone action and as catalysts. See also AAQ218330-Q21832
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                                                                                                                                                                                                                                                                                                                                                                        1008 TCTGGATTCCATTGCGACGACGACGACGACGTTAGCTATAGCTCTGTGGATGATGT 1067
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                                                                                                                                                                                                                                                                                                                                 CGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGG 1007
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                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                            New method of systematic polypeptide evolution by reverse translation by linking each polypeptide in sample mixt. to individualised mRNA allowing further synthesis of selected polypeptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                  182 cáacdacdacdacdacdacdacdacdacgacgacgacgacgacgacgacgacga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Systematic peptide evolution by reverse translation; SPERT; ligand; specific; inhibitors; probes; assay; cell sorting; ss.
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                    Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer for 5' fixed sequence contg. T7 promoter and RBS
                                                                                                                                                                                                                                                                      0; Mismatches 187; Indels
                                                                                                                                                                                                                             Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                  Score 66.8; DB 2;
Pred. No. 3.5e-05;
                                                                                                     Example, Page 55; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ36859 standard; DNA; 390 BP.
                                                                                                                                                                                                                                                  3.1%;
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(first entry)
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                                                                                                                                                                                                                                                                    Matches 179; Conservative
                                         WPI; 1992-080018/10
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                                                                                                                                                                                                                                                            Local Similarity
                     Tuerk C;
                                                             New method of
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                     Gold L,
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Synthetic.

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SPERT is used to select novel polypeptides that bind the antibody of the epitope commonly recognised by the antisera from autoimmune mice which are the fi progeny of a cross of NZB and NZW parents (Portanova et al., J. Immunol. 144, 4633, 1990). The known epitope consists of ca. 10 amino acids at the N-terminus of the histone HZB protein. To make mRNA encoding candidate polypeptides a 5' fixed sequence composed of a 7' promoter sequence and a ribosome binding site which is recognised by both provaryotic and eukaryotic ribosomes, terminating in a restriction prokaryotic and eukaryotic ribosomes, terminating in a restriction prokaryotic and eukaryotic ribosomes, terminating in a restriction provate stee is synthesised and cloned using a number of oligonuclectides (example shown). A 3' fixed sequence is placed into a restriction site to provide an mRNA encoding the C- terminal trailer sequence of ca. 100 nucleotides lacking stop codons. In addition, a 3' primer annealing site is provided so that cDNA synthesis can be accomplished on the mRNA recovered from partitioned ribosome complexes. See also AAQ36845-63. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                  Systematic polypeptide evolution by reverse translation - used for prodn. of polypeptide ligand specific for desired target molecule.
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48.9%; Pred. No. 3.5e-05;
ive 0; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                             Smith
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                                                                                                                                                                                                                      Tuerk C, Pribnow D,
92WO-US000801
                                                                         91US-00739055
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                                                                                                                                               (UYRE-) UNIV RES CORP
                                                                                                                                                                                                                                                                                            WPI; 1993-076529/09.
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Matches 179; Conserv
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AAF76910
ID AAF7
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182 1128 242

CACCACGCCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGGGAGACGGACAGTGCATCCTC 1187

1188 AGCCTCAAATGATGACAATGTGTTCGATGACTTTACCAGCTACAATGCCCACAAAAAGAA 1247

1248 GCAGGA 1253

CGACGA 367

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolating a polypeptide ligand to a target molecule, useful for diagnostic assays, comprises partitioning candidate mixtures comprised of ribosome complexes or mRNA.polypeptide copolymers relative to their affinity to the target molecule.
                                                                                                                  ligand isolation; systemic polypeptide evolution by reverse translation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drugs, metabolites, cofactors and toxins. Polypeptide ted and rapidly identified by this method
                                                                                  Sequence containing a 120 repeat of ACG flanked by fixed fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.1%; Score 66.8; DB 5; Length 390; 48.9%; Pred. No. 3.5e-05; ive 0; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Col 39; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pribnow D,
                                                                                                                                                                                                                                                                     98US-00197649.
                                                                                                                                                                                                                                                                                                     90US-00561968.
                                                                                                                                                                                                                                                                                                                   91US-00739055.
                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-243412/25.
                                                                                                                                                                                                                                                                                                                                                                       GOLD L.
TUERK C.
PRIBNOW D.
SMITH J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuerk C,
                                                                                                                                                                                                  US6194550-B1
                                                                                                                                                                                                                                                                     23-NOV-1998;
                                                 29-MAY-2001
                                                                                                                                                                                                                                                                                                                   01-AUG-1991
                                                                                                                                                                                                                                  27-FEB-2001
                                                                                                                                                                   Synthetic.
               AAF76910;
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                                                                                                                                                                                                                                                                                                                                                                     (GOLD/)
(TUER/)
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The sequences given in AA172769-81 are oligonuclectides which were used to make mRNA encoding a candidate polypeptide, a 5' fixed sequence composed of a 17 promoter sequence and a ribosome binding site which is recognised by both prokaryotic and eukaryotic ribosomes, terminating in a restriction endonuclease site. The resulting nucleic acid was used in the method of the invention for preparing ligands of target molecules in which mixtures of ribosome complexes or mRNA.circle-solid.polypeptide copolymers (mRcs.pCs) are partitioned by affinity to the target and amplified to create candidate mixtures enriched in ribosome complexes or mRs.pCs with an affinity to the target, are new. The methods are termed SPERT (Systematic Polypeptide Evolution by Reverse Translation). The SPERT methods are useful for isolating polypeptide ligands for desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New methods (termed SPERT (Systematic Polypeptide Evolution by Reverse Translation)) for selecting high-affinity polypeptide ligands that specifically bind target molecules, e.g. proteins, carbohydrates, toxins,
                                                                                                                                                   T7 promoter; ribosome binding site; RBS; prokaryotic; eukaryotic; ribosome; mRNA.circle-solid.polypeptide copolymer; mRcs.pC; SPERT; Systematic Polypeptide Evolution by Reverse Translation; assay; diagnosis; cell sorting; inhibitor; probe; sequestering agent;
                                                                                                                    Oligo #7 for cloning T7 promoter and RBS containing mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 21; 38pp; English.
                 AAI72775 standard; DNA; 390 BP.
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91US-00739055.
98US-00197649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pribnow D,
                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2001; 2001US-00790399
                                                                                  (first entry)
                                                                                                                                                                                                                             ribosome complex; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-329128/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drugs and receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOLD L.
TUERK C.
PRIBNOW D.
SMITH J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuerk C,
                                                                                                                                                                                                                                                                                              US2002038000-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-1998;
                                                                                    22-JUL-2002
                                                                                                                                                                                                                                                                                                                                  28-MAR-2002
                                                                                                                                                                                                                                                             Synthetic.
                                                  AAI72775;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PRIB/)
(SMIT/)
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AAI7277
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Gaps

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61

CGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGG 1007

888 GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT 947

Best Local Similarity 48.9 Matches 179; Conservative

0 948 62

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1008 TCTGGATTCCATTGCGGACGACGACGACGACGTTAGCTATAGCTCTGTGGATGATGT 1067

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target molecules. The polypeptide products are useful for any purpose to which a binding reaction may be put, for example in assay methods, confagnostic procedures, cell sorting, as inhibitors of target molecule function, as probes, as sequestering agents and the like. In addition, confactures include natural and synthetic polymers, including proteins, collypeptide products of the invention can have catalytic activity. Target molecules include natural and synthetic polymers, including proteins, complexite acids, and small molecules such as drugs, metabolites, cofactors, transition state analogues and toxins. The novel SPERT method involves utilizing a candidate mixture of polypeptides having a randomized amino acid sequence. Each member of the mixture is linked to an individualized mRNA, which encodes the amino acid sequence of that polypeptide in property of candidate polypeptides are partitioned according to their property of candidate polypeptides are partitioned according to their property of binding to a given desired target molecule. The partitioning is carried out in such a way that each mRNA encoding a polypeptide is partitioned exactly together with the means for further amplifying it by an in vitro process. Ultimately, both the desired optimal polypeptide are considered and further synthesis of the selected allowing further synthesis of the selected collypeptide as desired, and further synthesis of the selected collypeptide selected polypeptide (using protein chemistry) in order to produce it in a charities.
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(SYGN) SYNGENTA PARTICIPATIONS AG

22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105

WO2003000898-A1

03-JAN-2003

Oryza sativa

Length 390; Score 66.8; DB 6; Length 3 Pred. No. 3.5e-05; 0; Mismatches 187; Indels Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 U; 0 Other; 3.1%; Query Match

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1067 CGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGG 1007 CACCACGCCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCATCCTC 1187 1188 AGCCTCAAATGATAACAATGTGTTCGATGACTTTACCAGCTACAATGCCCACAAAAAGAA 1247 888 GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT 947 241 1008 TCTGGATTCCATTGCGGACGACGACGACGACGTTAGCTATAGCTCTGTGGATGATGT Gaps ö Best Local Similarity 48.9 Matches 179, Conservative 1248 GCAGGA 1253 CGACGA 367 948 242 1128 62 362 ò 임 ò 셤 ò g g g ò ठ à 셤

ADA71938 standard; DNA; 2000 BP. (first entry) Rice gene, SEQ ID 5263 20-NOV-2003 ADA71938;

Plant, bacterial infection; fungal infection, viral infection; rice, gene, ds.

involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant present invention relates to a method (M1) for identifying genes ö Hou Y; Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other; SA, Zhu Glazebrook J, Goff Whitham S, Xie Z, Claim 27; SEQ ID NO 5263; 899pp; English κ'n Cooper ; invention Chen W, Co WPI; 2003-175290/17 gene expression illustrate the Œ, Chang H, Katagiri

3, ACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGGTC 1009 312 769 829 132 72 193 KRMWMSSCGRSGCGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRAYMTTSYSWACSSYT 13 SSWRGRRRMYMAGMMSCARMGSRRMSRKMGSMSKYRKCSSCGKCKMTTRRKSKWYSASSA 710 GCACGGCGACCGCCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTTGGGGTTCATCG 770 GICTGGGGCTGGTCGTTGCCATTCTCGCACTAACGATCTGGCAGACACGCGTGTATCGC ATCTGGACAAGGAGCTGAAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTTGG 890 GCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCG Gaps 8 3.1%; Score 66.4; DB 7; Length 2000; 10.0%; Pred. No. 8.5e-05; 415; Mismatches 391; Indels Local Similarity 10.0% es 90; Conservative 950 Query Match Best Loca Matches В 8 ò ద 셤 ò ò 셤 ò g 1069

GCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCA 1129

CCACGCCCACATCTGAGACCACTGAGGGCGAGGGCGAGACGGACAGTGCATCCTCAG

TGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGATGATGTTG

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(BALL/) BALLESTAS M E.
(KAYE/) KAYE K M.
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                                     1250 AGGAGAGAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAA 1309
                                                                         1310 ATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAGAGAGCCCTGCAC 1369
                                                                                                             1370 CACTTCACCACCGTCGCAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGCCA 1429
                                                                                                                                                  1430 GATCCGAGGACTCGAGGCCAGCAGCCCATTTCCACTTGAGCAGCAGCGGCGTCACCAAG 1489
                                                                                                                                                                                     GAAGTATGGGCTACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAACTCTTATC 1549
                                                                                                                                                                                                                         AGGGACACTTTCAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACG 1609
                                                                                                                               727
                                                                                                                                                                                                788 YWWYWRIYMKMYKMYKCIKIYWYWSAIYWIGIWAAW---WMAKIKMRMGMIGAKIRGR 844
                                                                                                                                                                                                                                    latency-associated nuclear antigen; LANA; gamma-2 herpes virus;
Human herpes virus 8; HHV8; rhadino virus cis-acting element; RVCAE;
Kaposi's sarcoma; primary effusion lymphoma; PEL;
human immunodeficiency virus; HIV; multicentric Castleman's disease; ds.
                                                                                                                         669 YYMSKYTYAKYGSYMRYRYRAM-CMYMWRNYYRYRSYMTYMAWYISSTRMAMTGMKYSG
                                                                                                                                                             128 RYWTSWYKYCKCSWKYRSMWYYWSWWWAKTWKWWRRYATRWMWWYRYSWKWYTWCTMWG
            549 YYWAGMWMKRYKRMYKRMWWWKRKYSKCSWYCKMSYYASCMKSARKAGAKMCKRSKMS
                                                                                  Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;
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/*tag= b
hote= "nuclear localisation signal, NLS"
190. .210
/*tag= c
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/note= "nuclear localisation signal,
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1. .3489
/*tag= a
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40. .50
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99US-00298568
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21-APR-1999;
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11-SEP-2000
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(KSHV) latency-associated nuclear antigen (LANA) gene. KSHV is also known as Human Herpes virus 8 (HHV8) and belongs to the rhadino virus, or gamma 2 herses virus class. The LANA protein is necessary for the efficient persistence of rhadino virus DNA in mammalian cells. Persistent rhadino virus infection is implicated in a variety of diseases e.g. Kaposi's Sarcona (KS). Primary Effusion Lymphoma (PBL) and multicentric Carleman's disease. In addition, KS is a common malignancy in HIV patients. KSHV persists in host cells in a latent form. One of the few genes expressed from the latent viral DNA is LANA associates with choth human chromosomes and with the rhadino virus cis-acting element (RVCAB), thereby providing a tethering function: the KSHV DNA episome is "tied" to the host chromosomes. This allows the viral DNA to persist in the latent inhibit LANA interaction with RVCAB, thereby interfering with the latency cycle of this virus. Potential antiviral treatments for the above mentioned diseases may therefore be based on LANA deregulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating or preventing a disease associated with rhodino virus infection in a mammal which includes Kaposi's Sarcoma and Primary Effusion
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                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is the Kaposi's sarcoma-associated herpesvirus
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Pred. No. 0.027;
0; Mismatches 132; Indels
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Kaye KM
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Best Local Similarity 50.6%;
Matches 135; Conservative 0
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Ballestas ME,
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                                                                            WPI; 2000-387829/33.
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29-JUN-2001
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The invention provides a composition comprising nucleic acid, histone HI forcein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the tethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone HI. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone HI and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, Parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Kaposi's sarcoma associated herpesvirus (human herpesvirus 8) latency-associated nuclear articus multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A composition for use in gene therapy comprises an expression vector that includes a nucleic acid binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              947
Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8; KSHV; latency-associated nuclear antigen; LANA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen (LANA), which acts as a tethering protein. (Updated on 06-AUG-
2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS
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                                                                                               Location/Qualifiers
1. .3489
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                                                           herpesvirus 8.
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nes 135; Conserv
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987 GGATGATGAGGAGGAGCAGAGACAGATGAGGAGGACGAGGATGACGAGGATGA 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an episome in mammalian cells, comprising the rhadinoviral sequence LANA (latency-associated nuclear antigen) of 3489 base pairs (see ABA93487, $1) expressed in the cell, and the rhadinoviral sequence RVCAB (rhadinoviral cis-acting element) of 801 base pairs (see ABA93488, $2) present in the plasmid. Also describes is a method for maintaining a closed circular DNA in a cell by expressing (S1) in the cells and having particularly used in gene therapy (or other gene transfer applications) that uses mammalian cells in which LANA is expressed. (A) improves persistence of gene therapy vectors in cells. The present sequence encodes Kaposi's sarcoma-associated herpesvirus (KSHV, also called human herpesvirus 8) LANA protein, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                System for episomal retention of plasmids in mammalian cells, useful in gene therapy, comprises rhadinoviral LANA and RVCAE sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          828 GCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTT
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                                                                                                                   Kaposi's sarcoma-associated herpesvirus LANA protein encoding DNA.
                                                                                                                                                      Kaposi's sarcoma-associated herpesvirus; KSHV; LANA; RVCAE; PEL; KSHV terminal repeat; rhadino virus cis acting element; episome; primary effusion lymphoma; latency-associated nuclear antigen; gene therapy; gene transfer; gene; ds.
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Pred. No. 0.027;
0; Mismatches 132; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                 /note= "latency-associated nuclear antigen"
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/*tag= a
/product= "LANA protein"
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                  BP.
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              ABA93487 standard; DNA; 3489
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les 135; Conservative
                                                                                                                                                                                                                                              Human herpesvirus 8.
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P-PSDB; ABB05621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention
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                                                                                    25-APR-2002
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This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORFS which encodes capsid protein IV, ORF67, which encodes tegument protein IV, ORF68 which encodes a glycoprotein, ORF99, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D, ORF73 which encodes immediate early protein (IEP), K14 which encodes (V-adh), ORF74 which encodes G-protein coupled receptor, ORF75 which encodes tegument protein/FGARAT, K15. KSHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neocuring in persons with acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated with Kaposi's sarcoma in a
                                                                                                                                                                                                                                                                                                                                      Kaposi's sarcoma, acquired immune deficiency syndrome, AIDS, DHFR, Bcl-2; dihydrofolate reductase, LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HHVB; capsid protein IV; tegument protein IV; glycoprotein; kaposin; cyclin D; immediate early protein; IEP; OX-2; v-adh; G-protein coupled receptor; FGARAT; ds.
                                           TCTGGATTCCATTGCGGACGACGACGACGACGTTAGCTATAGCTCTGTGGATGTGT
                                                                      or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
di:hydro:folate reductase and is useful for treatment, prophylaxis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting expression of a DNA virus associated with Kacell. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                             KSHV LUR DNA (nucleotides 105,301-137,507).
                                                                                                                            GGACAATGAGGACGAGGAGGATGACGA 1253
                                                                                                    TGGCGCAGACTACGAGGACTACACCGA 1094
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AAV73805 standard; DNA; 32207 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis of Kaposi's sarcoma.
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                                                                                                                                                                                                                 CGACTATCCAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGG
                                                                                                                                                                                                                                                                                    20890 CGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGAGGATGACGAGGAGGA
                                                                      GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT
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90173. .90643
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complement (17261. .17875)
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complement (69412. .69915)
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complement(88410. .88910)
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/product= "interleukin 6"
complement(21548. .21832)
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complement (58976. .60175)
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Best Local Similarity 50.6 Matches 135; Conservative

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This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known as human herpes virus 8 (HHVB). This sequence contains the DNAs of the invention which encode KSHV polypeptides selected from: (a) viral invention which encode KSHV polypeptides selected from: (a) viral invention which encoded by Complement-binding protein; glycoproteins B, M or L; C (a) viral IRF ; (d) complement-binding protein; glycoproteins B, M or L; C (d) train IRF i, (d) complement-binding protein; glycoproteins B, M or L; C (d) train IRF i, (d) complement-binding protein; glycoproteins B, M or L; C (d) train IRF i, (d) complement-binding protein; glycoproteins B, M or L; C (d) capsid protein IV encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by it and antibodies (Ab) specific for the proteins are useful for c detecting HHVB, specifically for diagnosis of Kaposi's sarcoma, in body cor triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHVB infection, while the protein can be used in protective vaccines. Ab may also be used for prophylaxis or treatment of HHVB infection, cother lymphoproliferative diseases such as lymphomas, leukaemia, contening the nucleic acid are useful for grang screening. HHVB-derived peptides can be cused as targets for antiviral drugs, e.g. dihydrofolate reductase gene cused as targets for antiviral drugs, e.g. dihydrofolate reductase gene the immune status of a patient infected with HVY. HVB derived protein cviral MIP III may be used as an anti-inflammatory agent for, e.g. treating rheumatoid arthritis. This sequence is stated as containing 81 containing 81 containing Frames. (Updated on 27-MUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding Kaposi's sarcoma associated herpes virus proteins – useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients.
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                                                            /product= "interferon regulatory factor 4" complement (111931. .112443)
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/product= "immediate early protein"
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      /product= "glycoprotein X"
complement(93636. .94127)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UYCO ) UNIV COLUMBIA NEW YORK
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96US-00686349.
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13-NOV-1996;
13-NOV-1996;
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25-JUL-1996;
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828 GCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTT 887

0; Gaps

Score 55.8; DB 2; Length 137507; Pred. No. 0.12; 0; Mismatches 132; Indels 0;

Query Match 2.6%; Best Local Similarity 50.6%; Matches 135; Conservative

Query Match

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126250 CAAGAAGATGACGAGGAGGATGACGAGGATGACGAGGATGACGAGGAGATGA 126191
                                                                                                                                126190 CGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGA 126131
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888 GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT 947
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Sequence 1, Appli
Sequence 20, Appl
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Sequence 10, Appl
Sequence 112, Appli
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6659.411 Million cell updates/sec
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                                                                                                                  2148
                                                            ; Search time 179 Seconds
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                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-728-323A-1
US-09-298-568-1
US-09-298-568-1
US-09-17-659A-20
US-08-770-379-20
US-08-770-379-20
US-08-770-379-20
US-09-230-371A-20
US-09-489-847-112
US-09-489-847-112
US-09-413-574-1
US-09-413-574-1
US-09-182-816-22
US-09-182-816-22
US-09-182-816-22
US-09-182-816-22
US-09-183-37-1
US-09-634-530-24
US-09-634-530-24
US-09-634-530-24
US-09-634-530-1
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US-09-634-537-1
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                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                             682709 segs, 277475446 residues
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                                                            September 14, 2004, 19:37:16
                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
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seq length: 200000000
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Match 1
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Maximum DB
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Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 16317, A
Sequence 16317, A
Sequence 16324, A
Sequence 11, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Sequence OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed OTHER INFORMATION: fragments having Ncol restriction sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1%; Score 66.8; DB 3; Length 390; 48.9%; Pred. No. 3.9e-07; tive 0; Mismatches 187; Indels (
          US-08-340-820-24
US-08-591-535-24
US-08-747-2218-24
US-09-005-051-24
US-09-005-051-24
US-09-005-051-26
US-09-403-942F-24
US-09-403-942F-26
US-09-403-942F-26
US-09-621-976-16324
US-09-621-976-16324
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US-09-621-976-16324
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US-09-621-976-16324
US-09-621-976-16324
US-09-611-410-1
US-09-611-411-9
US-08-461-441-9
PCT-US-93-08518-9
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ORGANISM: Artificial Sequence
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nes 179; Conservative
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Batent No. 6482887
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
FILE REFERENCE: UM-03778
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kieff, Elliott D.
APPLICANT: Kafeff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
TITLE OF INVENTION: HAMDINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-1001R
CURRENT APPLICATION NUMBER: US/09/298,568
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER PILING DATE: 1998-11-19
                                                                                                                              1008 TCTGGATTCCATTGCGGACGACGACGACGACGTTAGCTATAGCTCTGTGGATGATGT
                                          CGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
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Matches 135, Conservative
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                                                                                               1188 AGCCTCAAATGAGAAATGTGTTCGATGACTTTACCAGGTACAATGCCCACAAAAAGAA
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llarity 50.6%; Pred. No. 0.00063;
Conservative 0; Mismatches 132; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Relaman, Isidore S.
APPLICANT: Moore, Partick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA TITLE OF INVENTION: Encoding Same And Uses Thereof NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
CLASSIFICATION: 435
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPREBRENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEDHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08728323A Patent No. 5948676 GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
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EDNESS: single
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STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10036
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US-08-728-323A-1
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Best Local S:
Matches 135
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TOPOLOGY:
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Patent No. 5849564

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Edelman, Isladore S.
APPLICANT: Edelman, Isladore S.
APPLICANT: Accelman, Isladore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                         2.6%; Score 55.8; DB 4; Length 3489; 50.6%; Pred. No. 0.00063; Live 0; Mismatches 132; Indels 0
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1068 TGGCGCAGACTACGAGGACTACACCGA 1094
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CURRENT APPLICATION NUMBER: US/09/410,399 CURRENT FILING DATE: 1999-10-01 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin Ver. 2.0
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1185 Avenue of the Americas
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234;
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 291-0525
INPORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                              Best Local Similarity 50.6
Matches 135; Conservative
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CLASSIFICATION: 435
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STATE: New York
COUNTRY: U.S.A.
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                                                                                    SEQ ID NO 1
LENGTH: 3489
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20950 CGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGA 20891
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                                                                                                                                                                                 Query Match 2.6%; Score 55.8; DB 2; Length 32207; Best Local Similarity 50.6%; Pred. No. 0.0019; Matches 135; Conservative 0; Mismatches 132; Indels 0;
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Busso, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20770 GGACAATGAGGACGAGGAGGATGACGA 20744
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELEFAN: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/757,6697
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; Sequence 20, Application US/08757669A
Patent No. 6183751
; GENERAL INFORMATION:
                                                                                                            DNA (genomic)
LENGTH: 32207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                          double
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                           TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                     linear
                                                                                                            MOLECULE TYPE:
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                                 ; TYPE: nuc:
; STRANDEDNES;
; TOPOLOGY:
; MOLECULE TYPE
US-08-770-379-20
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APPLICANT: Nakagawa Satoshi
APPLICANT: Sakaki yoshiyuki
APPLICANT: Zhao Nanding
APPLICANT: Hashida Hideji
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
TITLE OF INVENTION: AND NOVEL ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE KEREKKULE: KOJOLELE:
CURRENT PEDELICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-06
SARLIER PLING DATE: 1998-08-06
                                                                                                                        20770 GGACAATGAGGACGAGGAGGATGAGGA 20744
                                                          1068 TGGCGCAGACTACGAGGACTACACCGA 1094
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-112
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                                                                                                                                                                                                                                                                                                                                         Sequence 112, Application US/09489847
Patent No. 6476195
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Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: SITE
LOCATION: (946)
PURER INFORMATION: INFORMATION
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LOCATION: (936)
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APPLICANT: Chang, Yuan
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1997-07-22
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                                                                                                                                                          Score 55.8; DB 3; Length 32207;
Pred. No. 0.0019;
0; Mismatches 132; Indels 0;
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Sequence 20, Application US/09230371A
Patent No. 6348586
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20
                                                                                                                                                          Query Match
2.6%;
Best Local Similarity 50.6%;
Matches 135; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%;
Best Local Similarity 50.6%;
Matches 135; Conservative
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US-09-230-371A-20
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) NAME/KEY: CDS
; LOCATION: (58)...(1272)
US-09-413-574-1
                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea maye
                                                                             US-09-621-976-10211
  SEQ ID NO 10211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-372-422A-39
                      LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10211. Application US/09621976
Fatent No. 6639063
GRENRAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                     CITY: New York
COMPUTE: New York
COMPUTE: New York
COMPUTE: New York
COMPUTE: State State State
COMPUTE: State State State
COMPUTE: State State
COMPUTE: State
CLASSIPICATION NUMBER: US/08/909,965C
FILING DATE: Aduat 12, 1997
CLASSIPICATION NUMBER: DCT/JP96/03630
FILING DATE: 12-No. 5936078-1995
ATDONEY/AGENT INFORMATION:
NAME: Lawrence S. Perry
NAME: Lawrence S. Perry
NAME: REGISTRATION NUMBER: 31865
                                         CELLA, HARPER AND SCINTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELERAX: 212-758-2982
TELEX: 236262
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3527 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
TELEPHONE: 212-758-2400
TELEFAX: 212-758-2982
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK,
STREET: 277 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 140 to 1084
LDENTIFICATION METHOD:
US-08-909-965C-7
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: human
IMMEDIATE SOURCE:
CLONE: F998
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US-09-621-976-10211
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2042 GGAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAAATATAT 2101
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                                                                                                                                                  179 TTAAAAGCAGTATGGGAACCAAATTTTTGTAAAGTAATATTTTCAACCTTTAAAAAAA
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Score 50.6; DB 4; Length 299; Pred. No. 0.0036; 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Malalan, Pramod B.

APPLICANT: Agaliani, Laura

TITLE OF INVENTION:

FILE REFRENCE: 0964

CURRENT APPLICATION NUMBER: US/09/413,574

CURRENT APPLICATION NUMBER: 60/109,728

EARLIER APPLICATION NUMBER: 60/109,728

EARLIER FILING DATE: 1998-11-23

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FREUSEQ for Windows Version 3.0

SEQ ID NO 1

LENTH: 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/09372422A
Patent No. 6313375
GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT APPLICATION NUMBER: US 60/098,692
PRIOR APPLING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-413-574-1
; Sequence 1, Application US/09413574
; Patent No. 6235972
     2.4%;
Query Match
Best Local Similarity 65.5%
Matches 74; Conservative
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Matches 92; Conservative
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TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES, TITLE OF INVENTION: PROTEINS AND USES THEREOF FLEARENERS: FC-3-CL CURRENT APPLICATION NUMBER: US/09/182,816 CURRENT FILING DATE: 1998-10-29 EARLIER APPLICATION NUMBER: 08/989,510 EARLIER FILING DATE: 1997-12-12 NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver. 2.0 SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 15, 2004, 02:20:54 Job time: 181 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-471_528-22
; Sequence 22, Application US/09471528
; Patent No. 6153397
                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-182-816-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Ctenocephalides felis
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Best Local Similarity 68.0'
Matches 70; Conservative
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; LOCATION: (159)..(1553)
US-09-471-528-22
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LENGTH: 1736
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                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-182-816-22
; Sequence 22, Application US/09182816
; Patent No. 6143542
; GENERAL INFORMATION:
; APPLICANT: Wisnewski, Nancy
; APPLICANT: Silver, Gary M.
; APPLICANT: Lo, Katherine C.
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: PROTFINS AND USES THEREOF
; TITLE OF INVENTION: WOWELE LO. 99, 182, 816
; CURRENT APPLICATION NUMBER: US/09/182, 816
; CURRENT APPLICATION NUMBER: 08/989,510
; EARLIER PILING DATE: 1999-10-29
; EARLIER PILING DATE: 1997-12-12
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NOS: 31
; SEQ ID NOS: 31
; SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 49
SOFTWARE: FRSICSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-182-816-24/C
; Sequence 24, Application US/09182816
; Patent No. 6143542
; GENERAL INFORMATION:
; APPLICANT: Wisnewski, Nancy
; APPLICANT: Silver, Gary M.
; APPLICANT: Lo, Katherine C.
; APPLICANT: Brandt, Kevin S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Ctenocephalides felis
                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (133) ... (1015)
US-09-372-422A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , LOCATION: (159)..(1553)
US-09-182-816-22
                                                                             TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                    FEATURE
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2040 GAGGAAAATCATATTTATTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAAATAT 2099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Wisnewski, Nancy
APPLICANT: Silvar, Gary M.

APPLICANT: Silvar, Gary M.

APPLICANT: Silvar, Gary M.

APPLICANT: Brandt, Kevin S.

TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
FILE REPRENCE: FC-3-C-1.

CURRENT APPLICATION NUMBER: US/09/471,528

CURRENT APPLICATION NUMBER: US/09/471,528

EARLIER APPLICATION NUMBER: 09/182,816

EARLIER APPLICATION NUMBER: 08/989,510

EARLIER PILING DATE: 1998-10-29

EARLIER FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 35

SOFTWARE PARENT NOS: 35
                                                       Gaps
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Query Match 2.3%; Score 50.2; DB 3; Length 1736; Best Local Similarity 68.0%; Pred. No. 0.011; Matches 70; Conservative 0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 1736;
                                                                                                                                                                                   2.3%; Score 50.2; DB 3; Length 1;
68.0%; Pred. No. 0.011;
ive 0; Mismatches 33; Indels
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Sequence 5, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 7734, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 483, App
Sequence 606, App
Sequence 9903, Ap
Sequence 38347, App
Sequence 38382, A
                                                                                                                                                                                                                                                                       (without alignments)
2527.528 Million cell updates/sec
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                                                                                                                                                                                                                              September 15, 2004, 00:00:21; Search time 4276 Seconds
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1: /cgn2 6/ptodata/2/pubpna/PCT_NEW_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-813-329-1
US-09-813-329-1
US-09-790-399-7
US-10-425-114-7734
US-10-424-599-46034
US-10-424-599-46034
US-10-294-804-1
5 US-10-214-864-1
5 US-10-214-863
US-10-424-599-9903
US-10-424-599-8903
US-10-424-599-89882
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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	Sequence 9339, Ap		Sequence 40658, A		Sequence 26900, A					Sequence 5966, Ap	881		112,	Seguence 2117, Ap		Seguence 59340, A	Sequence 33751, A		884,	Seguence 1931, Ap	5014	Seguence 118975,	Seguence 57216, A	Sequence 95204, A	Sequence 11054, A	Sequence 16481, A	Seguence 3380, Ap	31, Ag	38,	1989
US-03-814-323-17579	US-09-918-995-9339	US-10-424-599-6106	US-10-437-963-40658	US-10-311-455-1285	US-10-424-599-26900	US-10-437-963-24712	US-10-424-599-93967	US-10-424-599-116955	US-09-918-995-31149	US-10-021-323-5966	US-10-198-846-8818	US-10-767-701-11693	US-10-351-334-112	US-10-106-698-2117	US-09-960-352-6976	US-10-424-599-59340	US-10-424-599-33751	US-10-424-599-17202	US-10-374-780A-884	US-10-311-455-1931	US-09-960-352-15014	US-10-424-599-118975	US-10-437-963-57216	US-10-424-599-95204	US-10-021-323-11054	US-09-864-761-16481	US-10-424-599-3380	US-09-766-511B-31	US-10-241-220-38	US-09-814-353-19891
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52.4	52.4	52.4	52.4	52.4	25	51.8	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.4	51.4	51.4	51.2	51.2	51.2	51	51	51	51	51	51	51	51	51	51
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Sequence 5, Application US/09813329

Sequence 5, Application US/09813329

GENERAL INFORMATION

TITLE OF INVENTION: Veriants Thereof

TITLE OF INVENTION: Veriants Thereof

TITLE OF INVENTION Wariants Thereof

FILE REFERENCE: DOO16.np

CURRENT APPLICATION NUMBER: US/09/813,329

CURRENT PILING DATE: 2001-03-20

PRIOR FILING DATE: 2000-03-21

NUMBER OF SEQ ID NOS: 65

SCOTTWARE: Patentin Version 3.0

SEQ ID NO 5
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100.0%; Score 2148;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2148; Conservative 0; Mismatches
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ORGANISM: Drosophila melanogastor
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; NAME/KEY: CDS
; LOCATION: (634)..(1860)
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 2166
TYPE: DNA
ORGANISM: Drosophila melanogastor
                                                                                       ; NAME/KEY: CDS
; LOCATION: (652)..(1878)
US-09-813-329-1
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Qy 1921 CGACTGCTCGTGAATGCGATTCATCGCCAGCGTGAATCCATAGTTCGTAGTC 1980 Db 1939 CGACTGCTCGTGAATGCGATTCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTC 1998 Qy 1981 TTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATTAGTCAGAAGACGG 2040 Db 1999 TTAGTCACTCCAAACCTCAATCTCAATCGGAATCGTGCATTAGTCAGAAAAACGG 2058 Qy 2041 AGGAAAATCATTTTTTTTTTTTTTTTTTTTTTTTTTTTT	RESULT 3 US-09-813-329-3 US-09-813-329-3 US-09-813-329-3 Sequence 3, Application US/09813329 Patent No. US20020012968A1 GENERAL INFORMATION: Workland State of Description Title OF INVENTION: Workland Thereof TITLE OF INVENTION: Workland Thereof TITLE OF INVENTION: Workland Thereof TITLE OF INVENTION: Workland State of Description Title Of Description NUMBER: US/09/813,329 CURRENT APPLICATION NUMBER: US/09/813,329 CURRENT PLING DATE: 2000-03-21 CURRENT APPLICATION NUMBER: 0500-03-21 FRIOR APPLICATION NUMBER: 0501-90,816 FRIOR APPLICATION NUMBER: 0500-03-21 TOTHE DATE: 2000-03-21 TYPE: DATE: NUMBER OF SEQ ID NOS: 65 SEQ ID NOS: 65 SEQ ID NOS: 65 LENGTH: 1221 TYPE: DATE CORGANISM: Drosophila melanogastor FRANCE: DATE OBEST LOCATION: (1): (1218) US-09-813-329-3 GREVE LOCATION: (1): (1218) US-09-813-329-3 ATGACTGCCGAGACCCTCCAACCCCTAACAGACTGCCAACAGATGCTTTT 693 ATGACTGCCAACACCCTCCAACCCACACACACACACACATGATTCTT 60 ON 634 ATGACTGCCCAACACCCTCCAACCCACCACACACATGATTCTT 60 ON 640 CCGCCAACACACCACCACACACACACACACACACACACA	Db 61 CCGGCCAAAGCAACACAACACAACAAGCAACCAACCAAC

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615 CGACGACGATGAAGACGAAGAAGAAAAGTGATGT 650
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ORGANISM: Glycine max
                                                 Best Local Similarity
Matches 147; Conserv
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     US-10-425-114-7734
                                    Query Match
Best Local
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APPLICANT: Zhou, Yihua
APPLICANT: Shous Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OP INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7734
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PRIOR FILING DATE: 1992-01-31
PRIOR APPLICATION NUMBER: 07/739, 055
PRIOR FILING DATE: 1991-08-01
PRIOR APPLICATION NUMBER: 07/561,968
PRIOR FILING DATE: 1990-08-02
NUMBER: 0F SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7734, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 46034, Application US/10424599
Publication Wo. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REPERENCE: 39-21(5323)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 1269
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53.3%; Pred. No. 0.00029;
tive 0; Mismatches 123;
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      Score 57.2; DB 13;
Pred. No. 0.00024;
0; Mismatches 123;
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US-10-424-599-46034
2.7%;
ilarity 53.3%;
Conservative
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2.6%; Score 55.8; DB 15; Length 3489;
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Query Match

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Best Local Similarity 50.6%;
Matches 135; Conservative
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Best Local Similarity
Matches 79; Conserva
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US-10-225-567A-606
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                                                                                                                            APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: RIADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE CURRENT APPLICATION NUMBER: 10412-10001R
CURRENT FILING DATE: 2001-06-28
PRICA APPLICATION NUMBER: US 60/109,422
PRICA FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PALENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.6%; Score 55.8; DB 13; Length 3489; Best Local Similarity 50.6%; Pred. No. 0.0014; Matches 135; Conservative 0; Mismatches 132; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1. Application US/10294804; Publication No. US20030133948A1; GENERAL INFORMATION: APPLICANT: Robertson, Erle S. APPLICANT: Robertson, Erle S. APPLICANT: Cotter, Murray A. TITLE OF INVENTION: Methods to Inhibit or Enj TITLE OF INVENTION: Methods to Inhibit or Enj TITLE OF INVENTION: Methods to Inhibit or Enj TITLE OF INVENTION: to Genomic Host DNA; FILE REPERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,294, RIOR APPLICATION NUMBER: US/09/410,399
RIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARR: PALENTIN Ver. 2.0
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                                                                      Sequence 1, Application US/09894273
Publication No. US20040037847A1
GENERAL INFORMATION:
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TYPE: DNA
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Sequence 483, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEEBNBROCK, Christian
APPLICANT: BIEELIN, Kurt
ITLE OF INVENTION: Cytosine methylation
ITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination FILE REFERENCE: 5013.1014

CURRENT FILING DATE: 2002-12-16
PRIOR PELING DATE: 2001-07-02
PRIOR PELING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
SEQ ID NOS: 2424

LENGTH: 5306
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                                                                                                                        987 GGATGATGAGGAGGAGGAGGAGAACAGATGAGGAGGAGGAGGATGACGAGGAGGATGA 1046
                                                                                                                                                                                                                                                                                                      CGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGG 1007
                                                                                                                                                                                                                                                                                                                                                        1107 CGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGGAGGAGA 1166
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                                                                                                                                                                                      GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT
                                                                                                                                                                                                                                           1047 CGAGGAGGATGACGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGA
                                                                            828 GCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTT
                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-483
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Pred. No. 0.0014;
0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1227 GGACAATGAGGAGGAGGATGACGA 1253
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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TYPE: DNA ORGANISM: Glycine max
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LENGTH: 372
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APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-44-4
CURRENT APPLICATION NUMBER: 02/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 606
LENGTH: 1915
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Fublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
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US-10-424-599-9903
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OTHER INFORMATION: ungure at all n locations
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; Sequence 82347, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-606
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Best Local Similarity
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Sequence 38982, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323)B
FILE REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EENGTH: 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.5%; Score 52.8; DB 13; Length Best Local Similarity 71.9%; Pred. No. 0.0013; Matches 69; Conservative 0; Mismatches 27; Indels
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US-10-424-599-38982
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US-10-424-599-82347
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1988 CTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGGAGGAAAA 2047
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GENERAL INFORMATION:
JEDILCANT: Lee, John
JEDILCANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
TITLE OF INVENTION: Iniliae, James
TITLE OF INVENTION: INVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: INDEPTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: INDEPTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: INDEPTIFICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR PELING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-22
PRIOR PELING DATE: 2000-07-22
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PRIOR PELING DATE: 2000-07-22
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PELING DATE: 2000-07-22
PRIOR APPLICATION NUMBER: US 60/257,672
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FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
(CURRENT APPLICATION NUMBER: US/10/264,049)
(CURRENT TAPLICATION NUMBER: US/10/264,049)
(CURRENT FILING DATE: 2002-10-04)
(PRIOR APPLICATION NUMBER: PCT/US01/18569)
(PRIOR APPLICATION NUMBER: US 60/209,467)
(PRIOR PILING DATE: 2000-06-07)
(PRIOR FILING DATE: 2000-06-07)
(PRIOR FILING DATE: 2000-06-07)
(SOFTWARE: PALENTIN Ver. 3.1)
(SEQ ID NO 287)
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Pred. No. 0.0023;
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NAME/KEY: misc feature

LOCATION: (1895)...(1895)

OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-287
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; Sequence 17579, Application US/09814353
; Publication No. US20030165831A1
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ORGANISM: Homo sapiens
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ORGANISM: HOMO
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Search completed: September 15, 2004, 08:12:30 Job time : 4278 secs

Perfect score:

Sequence:

OM nucleic

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Scoring table:

Searched:

Minimum DB a

Database

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BG640917 SD12092.5
A1260099 LP03784.5
B1620499 RH91659.5
CK135986 SD18286.3
CK135525 RH51659.3
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B163592 SD17545.5
BX560278 BX560278
                                                                                                                                 BX560278 BX560278
BL108596 Dr08ophil
BG553000 Bd082099.
CD099002 AGENCOURT
BU711992 SJEEJA02
BU771992 SJEEJA08
BU771992 SJEEJA08
BU771992 SJEEJA08
BU76449 SJEEJA08
BU7644956 BU7CMCTTP
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CF147545 AGENCOURT
BU766490 BU74956 BU76956
BU165350 CETS66564
BU39390 TELTAOGON
BU165350 CETS66564
BM307698 BA732905.
C84767 CR4767 DICC
AL193990 TELTAOGON
BM165350 EST567756
BM160252 EST56775
BM160252 EST577765
BM160252 EST577765
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Drosophila melanogaster
Drosophila melanogaster
Brusaryota; Metazooa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 699)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003331: arm:2R [4876906,5137815]
estimated-cyto:46813-46E4: 04/13/2001
Plate: SD.156 row: A column: 11
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                         A1260099
B1520499
CK135525
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BX560278
CNS017WQ
BG553005
CD09026
BU771970
BQ524571
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CD752688
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AW134038
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AZ526485
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BW1249956
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BG636194 SD13795.5
BI637732 SD19794.5
BI638827 SD21218.5
                                                                                                                                 September 14, 2004, 18:37:56; Search time 8239 Seconds (without alignments) 7785.406 Million cell updates/sec
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                                                                                                                                                                                                                                                   2148
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                       5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                             27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                       GenCore version
Copyright (c) 1993 - 2004
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                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    summaries
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Maximum Match 100%
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2148
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Score

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686.4 678 673.4 666.8

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1461 CCACTTGAGCAGCAGCGGCGTCACCAAGGAAGTATGGGCTACCATGGAGATATGTACAT 1520
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Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture_porz"
                46E1-46E1;: 04/13/2001, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 A. Stour C. Stou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GACGGTGACCAATACAGGCCTATATTACGCATATACGCCCAGATATGCTACAACTAGCTA
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
/mol_type="mrNA"
/db xref="taxon:7227"
/clone="SD13795"
                      2R
                                                                                                                                                  Drosophila melanogaster (fruit fly)
                      on:
                FBan0012919 located
                                                                                                                                                                              Drosophila melanogaster
                                                                                               GI:13763731
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                                                                                            BG636194.1
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              CG12919: F
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                                                                                                     /mol_type="mRNA"
/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone="SD15611"
/lab_host="DH5-alpha"
/clone lib="SD brosophila melanogaster Schneider L2 cell
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                                                           1. .699
/organism="Drosophila melanogaster"
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quality sequence stop: 698
Location/Qualifiers
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BG636194 686 bp mRNA linear EST 23-APR-2001 SD13795.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD13795 5 similar to

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BI638827 527218.5prime SD Drosophila melanogaster Schneider L2 cell culture port Drosophila melanogaster Clone SD21218 5, mRNA sequence.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eveptera; Endopterygota; Ditera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.

1 (bases 1 to 688)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BOGP/HHMI Drosophila EST Project
Unpublished (2001)
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                                                                                   GTTTTTTTTTTTTTTTGGTTTTTCGCTGTGCCTTTATCGCAAACAAGAACTGATAAAAC
                                                                                                         G-TTTTTTTTTTTTTTGGTTTTTGGCTGTGCCTTTATCGCAAACAAGAACTGATAAAAC
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
hit gened cyto:46B13-46B4: 05/19/2001
Plate: SD.212 row: B column: 6
High quality sequence stop: 602.
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/mol_type="mRNA"
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                                                                                                                                                                                                           CTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGGAGAAAATCATATTTTT 2060
                                                                                                                          TCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTCTTAGTCACTCCAAACCTAAT 2000
                                                               481 CGGTCAGAAGATGGAATACCAGTTTAAGCTTTAGTCCCTGCGACTGCTCGTGAATGCGAT 540
                                                                                                                                                GCGTGCATGATAGCGAAGAAAAAGCTATCCGTTTCAGTTAACTACTTACCAAGATTGA 129
                                                                                                                                                                                                                                   601 CTCAATCGGAATCGTGCATACTTGCATAGTCAGAAGACGGAGGAAAATCATATTTTT 660
GGAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTGTAAATTGGAGAGATTATCCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Brusrycta: Metazoda; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilae; Drosophila.
I (bases 1 to 686)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
Broky, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
Broky, M.M. Drosophila EST Project
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/clone lib="SD Drosophila melanogaster Schneider L2 cell
culture pOT2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46E4: 05/19/2001
Plate: SD 197 row: H column: 10
High quality sequence stop: 584.
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/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="SD19794"
                                                                                                                                                                                                                                                                                               2061 GTATATACTCGTTCGACTCTAAAAG 2086
                                                                                                                                                                                                                                                                                                                    661 GTATATACTCGTTCGACTCTAAAAG 686
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Best Local Si
Matches 685,
421
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KEYWORDS
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Mosptera, Endopterarygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 649)

1 (bases 2 to 649)

1 (bases 3 to 649)

1 (bases 3 to 649)

1 (bases 4 to 649)

2 (bases 4 to 649)

2 (bases 4 to 649)

3 (bases 4 to 649)

4 (bases 6 to 649)

4 (bases 6 to 649)

5 (bases 6 to 649)

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7 (bases 6 to 649)

8 (bases 6 to 649)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_type="mRNA"
/clone="SD12092"
/lab_host="DH5-alpha"
/clone_lih="SD brosophila melanogaster Schneider L2 cell
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Emal: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated cyto:46813 46851 04/13/2001
Plate: SD.120 row: H column: 8
High quality sequence stop: 597.
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                                                                                                                                                                                                    Contact: Stapleton, M.
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nes 646; Conserv
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/db xref="taxon:7227"
/clone="SD21218"
/lab.host="DH5-alpha"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture pOT2"
/note="Vector: pOT2; Site_1: EcoR1; Site_2: Xho1; Sized
fractionared cDNAs were directly ligated into pOT2.
Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                           CGCGTGCGTGCATGATAGCGAAGAAAAAGCTATCCGTTTCAGTTAACTACTTACCAAG 124
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BI620499 565 bp mRNA linear EST 07-SEP-2001
RH51659.5prime RH Drosophila melanogaster normalized Head pFlc-1
Drosophila melanogaster cDNA clone RH51659 5, mRNA sequence.
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Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 565)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, M., Chawpe, M., Chawez, C., Dorsett, V., Farfan, D., Frise, E.,
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanenavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and
                                                                                                                                                                                                                                      430 GGTTGTTCTGTGTGCTCGTGTAGTATCTTAAATACATAGAGTGTGTTCATATAAAGTGCG 489
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BamHI; Library was kindly generated by Piero Carninci at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RH Drosophila melanogaster normalized Head
pFlc-1"
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                                                                 310 AGAGAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAAGGGCACCATC
                                                                                                                                                  370 AGCAGCCCGAGGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATGCTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
ht genomic ABE03831: arm:2R [4876906,5137815]
estimated-cytc:46B13-46E4: 08/22/2001
Plate: RH.516 row: E column: 11
High quality sequence stop: 442.
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/mol type="mRNA"
/db xref="taxon:7227"
/clone="RH51659"
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/lab_host="DH5-alpha TonA"
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BDGP/HHMI RH Drosophila EST Project
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Contact: Stapleton, M.
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/lab_host="DHS-alpha"
/clone_lib="LP Drosophila melanogaster larval-early pupal
pOT2"
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Drosophila melanogaster cDNA clone LP03784 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Brusayota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 604)
Lewis, D. Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: whole body; Vector: pOT2; Site 1: EcoR1; Site_2: Xho1; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library.
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Enail: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS05033
Plate: 37 row: G column: 12
High quality sequence stop: 421.

High quality sequence stop: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                       TGCTCTAAGATCCCCAGTGTTCATCAATTATGACTGCCGAGACCCTCAAG 649
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                                                               TGCTCTAAGATCCCCAGTGTTCATCAATTATGACTGCCGAGACCCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.9%; Score 599.2; DB 9; Length 99.5%; Pred. No. 1.3e-65; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Drosophila melanogaster"
|mol_type="mRNA"
|db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="LP03784"
sex="male and female"
                                                                                                                                                                                                                                                                                                 AI260099.1 GI:3867624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 601; Conservative
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Best Local S
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                             LOCUS
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JOURNAL
COMMENT
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                                                                                                                                                                      RESULT 6
AI260099
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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a Xhol site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003831: arm.2R {4976906,5137815}
Plate: SD.182 row: H column: 2
High quality sequence stop: 456.
Location/Qualifiers
1. .508
/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1902
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                                                                                                                                                                                                                                                            /lab host="DH5-alpha"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture_pOT2"
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                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="SD18286"
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CK135525.1
EST.
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DEFINITION
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CK135525/c
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RIKEN. The library was normalized and excised using recombinase. Plasmid cDNA library."
                                                                                                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.

(Dases 1 to 508)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                   CGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTACCAAG
                                                                                                                                                                                                                                                                                             ATTGAATTTCGCCATCGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACTGTGT
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                                                                            565;
                                                                            Length
                                                                                                              1; Indels
                                                                        25.4%; Score 545.4; DB 12; 99.8%; Pred. No. 6.8e-59; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Unpublished (2001)
Other ESTs: SD18286.5prime
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BDGP
                                                                                                          546; Conservative
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Best Local Similarity
Matches 546; Conserv
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CK135985/c
LOCUS
DEFINITION
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JOURNAL
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2023

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BIG36564
SD18286.5prime SD Drosophila melanogaster Schneider L2 cell culture pOTZ Drosophila melanogaster CDNA clone SD18286 5 similar to CG12919: FBan0012919 GO:[] located on: 2R 46E1-46E1;: 05/19/2001,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH5-alpha"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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                         172 GTTCGTAGTACCTAGTCTTAGTCACTCCAAACCTAATCGGAATCGGAATCGCATACTG
                                                                                                                112 CATTAGTCAGAAGACGGAGGAAAATCATATTTATGTTGTTGTATATACTCCTTCGACTCTAAA
  1964 GTTCGTAGTACCTAGTCTTAGTCATCCCAAACCTAATCTCAATCGGAATCGTGCATACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 TACGAGAATGCCCTCATCGACTATCC-CAAAAGGTGGATGGCCTCACGGATGAGGAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawrence Berkeley National Lab
Cone Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46B4: 05/19/2001
Plate: SD.182 row: H column: 2
High quality sequence stop: 491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
                                                                                                                                                                               2084 AAGTGAATAAAATATATGTAGCTATTA 2111
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                                                                                                                                                                                                           52 AAGTGAATAAAATATATGTAGCTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:7227"
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Matches 489;
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                                                                                                                                                                                                                                                                                                                                                                          Diswrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46813-4684: 08/05/2002
Plate: RH.516 row: E column: 11
High quality sequence stopp: 382.
Location/Qualifiers
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                                       Eukaryota; Metazoa; Arrhropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 532)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Stapleton,M., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.B., Celniker,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCAAGGAGACACTCCATTCTTGCAGTGCTTGAACACGGTGCCCACCAACATCCCACATA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inote="Organ: head, Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using cre recomblinase. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RH Drosophila melanogaster normalized Head
pFlc-1"
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon,7227"
/clone="RH51659"
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99.0%; Pred. No. 3.2e-53;
iive 0; Mismatches 5;
                                                                                                                                                                                                                                                                 BDGP/HHMI RH Drosophila EST Project Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male and female"
/dev stage="Adult"
/lab_host="DHS-alpha TonA"
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                Other ESTs: RH51659.5prime Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 503; Conservative
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Best Local S
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BX560278
BX560278 Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tse49al0_plc, mRNA sequence.
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1 (bases 1 to 612)
1 Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Immilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the teetse fly Glossina morsitans morsitans and expression analysis of putative immune
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                                                                                                                                    125 ATTGAATTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCGTCTGTGT
                                                                                                                                                           185 GTTGTGTTTTTTTTTTTTTTGGTTTTTGGCTGTGCCTTTATCGCAAACAAGAACTGAT
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All clones with suffix qlc are reverse primer reads starting end of the cDNA all plc reads are from the 3, end.
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
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/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse49al0_plc"
/tissue_type="adult infected gut"
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Genome Biol. 4 (10), R63 (2003)
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Glossina morsitans morsitans
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BX560278.1 GI:33368472
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      AACAATGCACATACCGGCACCACGCCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAG 1170
                                                                                          1171 ACGGACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTCGATGACTTTACCAGCTAC 1230
                                                                                                                                                                                                                                                                      GAGCAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACT 1350
                                                                                                                                                                                                                                                                                                                                                            TCCAAAGAGAGCCCTGCACCACTTCACCACTGCGCAGAATGCATTCCCGGCCATCGCCAC 1410
                                                                                                                                                                                                                                                                                           AATGCCCACAAAAAAAAAGCAGCAGAAAAATCTCGCTCGATTGCCGATGTACGCAATGAG 364
                                                                                                                                                                                                                                                                                                                                                                                   TCCAAAGAGGCCTGCACCACTTCACCACCGTCGCAGAATGCATTCCCGCCATCGCCAC 484
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Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

( bases 1 to 447)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
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/clome_lib="SD Drosophila melanogaster Schneider L2 cell
culture_por2"
                           AACAATGCACATACCGGCACCACACATCTGAGACCACTGCTGAGGGCGAGGCGAG
                                                                                                                    ACGGACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTCGATGACTTTACCAGCTAC
                                                                                                                                                                                  Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 66798
http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46E4: 05/19/2001
Plate: SD.175 row: D column: 9
High quality sequence stop: 445.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.0%; Score 408.8; DB 12; Length 99.1%; Pred. No. 8.4e-42; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="SD17545"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI635992.1 GI:15538202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCTAGTCCG 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 99.1
422; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCTAGTCCG 495
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Best Local S
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DEFINITION

RESULT 11 BI635992 LOCUS

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ð q ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

source

FEATURES

Matches

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Gapв

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863 320 923

ORIGIN

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDN Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="embryo, stage 31-32"
| Tab host="DH10B (phage-resistant)" |
| /clone lib="NH10B (of Emb4" |
| /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1: |
| /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1: |
| /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1: |
| /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1: |
| /note="Organ: pcm | /note |
| /note= new | /note |
| /note | /note | /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 bp mRNA linear EST 09-APR-2001
dab82e09.y1 NICHD_XGC_Emb4 Kenopus laevis cDNA clone IMAGE:4203736
5′, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  321 CGTCRATAATCTCCCAGCAACGTTTGGGCATAAACWATCTCGACGAATACGACGATTTCCA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924 AAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGACGGATGA 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGTCGTCGATAATCTCCAGCAGCGTTTGGGCATAAACTATCTGGACGAGGAGGACGAG 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 CGTGACGATGATGATGACGACGATGATGACGACGATGATGATGATGACGATGATGAC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
1 (bases 1 to 468)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                            CGTCGATAATCTCCAGCAGCGTTTGGGCATAAACTATCTGGACGAGTTCGAGGAGTTCCA
                                                                                                                                                                                                                           GATCTGGCAGACAACGCGTGTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGT
                                            DB 29; Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 468;
                                                                                                               IndelB
                                                                                                            38;
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                                                                      ; Pred. No. 1.5e-05; 13; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:4203736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1%; Score 65.6; I
48.9%; Pred. No. 47;
                                        5.4%; Score 115.6; 72.0%; Pred. No. 1.5
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Location/Qualifiers
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                                                                              Similarity
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                                        Query Match
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BG553005
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TITLE
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KEYWORDS
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN37D20 of DrosBAC library from Drosophila melanogaster (fruit
                                                                      /note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1631 ACAACTCGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCATTCCTGCAGT 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTGAACACGGTGCCCACCAACATGCCACATAAGGTGCACACCTGCCACACGAGTGGTC 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1751 TGATCCACCTGGAACGAAACGAGGATCCATCTGAAGGACATTCACAACGATCGCAATG 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1811 CAGTICTGCGGGAGGGAAACAACCGAAGCTACTITGGCATCTICAAGGTGTAAATTGGAG 1870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 GCTTTCAAACTGTACCCACTAACATGTCACTGAAAATCCACCTTGTCATACGAGCGGTT 428
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/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                          1571 ATGCCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                 607 ATGGTGTCTTGACTATTCGCGAATCGGGTCTTTATGTTTATGTTTATGCTCAAGTATGTTATA
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 3.9e-07;
0; Mismatches 107; Indels
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/db_xref="taxon:7227"
/clone="BACN37D20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fly), genomic survey sequence. AL108596
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/plasmid="pBeloBAC11"
/note="end : T7"
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64.5%;
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Matches 194;
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Drs. Donald Brown and Liquan Cai

CDNA Library Preparation: CLONTECH

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM3253 rows, n column: 20

High quality sequence stop: 496.

Location/Qualifiers

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1. 752
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/db xref="taxon:8155"
/clone="INAGE:693958"
/clone="INAGE:693958"
/clone=lib="NICHD XGC Tad1"
/clone=lib="NICHD XGC Tad1"
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;
Site 1: Sii; Site 2: Sfi; S' and 3' adaptors were used in cloning as follows: S' adaptor sequence:
S'-CAGGCCATATGGCC-3, and 3' adaptor sequence:
S'-ATTCTAAAGGCCGAGCGCCGAATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, or T). Average insert size 1.6 kb (range 0.9-3.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD099026

752 bp mRNA linear BST 15-MAY-2003
AGENCOURT 14011375 NICHD XGC Tadl Xenopus laevis cDNA clone
TMAGE:6939285 5', mRNA sequence.
                                                                                                                                                                                                          1039 GACGTTAGCTATAGCTCTGTGGATGATGTTGGCGCAGACTACGAGGACTACACCGGTATG 1098
                                                                                                                                                                                                                                                                                                                 1099 TTAAATAAACTCAACAATGCACATACCGGCACCACGCCCACATCTGAGACCACTGCTGAG 1158
                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGAGGCGAGACGGACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTCGATGAC 1218
                                                   81 GATGATGACGACGATGATGATGATGACGACGATGATAAAGATGATGATGACGACGAC 140
                                                                                                                                                       141 GATGATGATAAAGACGATGATGACGATGATGACGACGACGATGATGACGACGATGATGA
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119 ITCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGGCCTCACG 978
                                                                                                                                                                                                                                                                                                                                                             261 GATGATGATGACGACGATGATGATGATGACGACGACGATGATGACGACGATGATGACGÁC 320
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
1 (bases 1 to 752)
NCI-CGAP http://www ncbi.nlm.nih.gov/ncicgap.
NCI-CAPP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                      GATGAGGAGGACGACGATGCGATGGTCTGGATTCCATTGCGGACGACGAGGACGAC
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Best Local Similarity 56.9
Matches 115; Conservative
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AUTHORS
TITLE
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COMMENT
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KEYWORDS
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954
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895 AACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTAT
                                                         387 AATGATGACGACGATGATGATGACGACGATGATAAAGATGATGATGACGACGACGACGATGAT
                                                                                                                                    955 CCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGGTCTGGAT
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

September 13, 2004, 10:21:32; Search time 57 Seconds (without alignments) 2027.402 Million cell updates/sec Run on:

US-09-813-329-6 2162 1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* .: geneseqp1980s:* : geneseqp1990s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		app			SUMMARIES	
Result No.	Score	Query Match	Length	DB	O.	scrip
	2162	100.0	409	Ŋ	AAU77718	Aau77718 Drosophil
(2)	2082.5	96.3	406	ហ	AAU77717	Aau77717 Drosophil
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4	1656	9.92	325	4	ABB67553	Abb67553 Drosophil
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8	141	6.5	428	Ŋ	ABG93245	
6	138.5	6.4	1192	ო	AAB18165	Aab18165 Plasmodiu
10	138.5	6.4	1883	4	ABB60038	Abb60038 Drosophil
11	137	6.3	330	ო	AAY70227	Aay70227 Human RNA
12	137	6.3	532	4	ABB67173	Abb67173 Drosophil
13	137	6.3	2175	4	ABB65698	Abb65698 Drosophil
14	135	6.2	330	4	AAU21828	Aau21828 Novel hum
15	135	6.2	330	4	AAU86946	Aau86946 Human DNA
16	135	6.2	330	7	ADC46469	Adc46469 Human neo
17	134	6.2	466	9	ABR52760	Abr52760 Protein s
18	133.5	6.2	3583	4	ABB64814	Abb64814 Drosophil
19	133	6.2	234	4	AAB94508	Aab94508 Human pro
20	133	6.2	2500	m	AAB18272	Aab18272 Plasmodiu
21	132	6.1	391	ഗ	ABP53104	Abp53104 Human ect
22	132	6.1	391	Ŋ	ABB09082	Abb09082 Human EDA
23	132	6.1	391	9	ABR42324	Abr42324 Human EDA
24	132	6.1	391	7	AB001928	Abo01928 Human EDA
25	132	6.1	391	7	ADC35224	Adc35224 Human TNF

WPI; 2002-195121/25. N-PSDB; ABK11680.

37 5 ABG32877 85 2 AAR95607 72 5 AAR95607 72 5 ABF73584 11 4 AAU37362 64 4 AAU15058 64 4 AAU15058 83 4 AB58891 74 6 ABC18980 74 6 ABU15913 74 6 ABM71209 75 ABG96386 87 6 ABR97551 87 6 ABR97551 87 7 ABG96386 87 6 ABR97531 87 7 ABG96386 87 6 ABR97531 87 7 ABG96386 87 6 ABR97531 87 7 ABG96386 88 6 ABR975493 89 7 6 ABR975493 80 7 ABG96386 81 8 ABG96386 81 8 ABG96386 81 8 ABG96386 81 8 ABG96386 81 8 ABG96386 81 8 ABG96386		Abg32877 Frog zinc Aar95607 RRP3 telo Aae33788 Human nuc Abg73584 Candida a Aau37362 Staphyloc Aau15058 Protein e Abb73188 Candida a Abb15913 Protein e Abm71209 Staphyloc Abm71209 Staphyloc Abm71209 Staphyloc Abm30575 A human E Abb30575 A human E	
		ABG32877 AAR95607 AAR95607 AAR37388 ABP73584 AAU37362 AAU15058 ABP73188 ABB58581 ABU18980 ABU15913 ABM71209 AAB73709 AAB73709 AAB73709 AAB73709	ABR47551 ABR92133 ADB75483 ABG96386 AAE18614 ABR47549
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		129 129.5 129.5 127.2 127.2 126.5 126.5 126.5 126.5 126.5 126.5	1255.5 1255.5 1255.5 1255.5 1255.5
	129 120 121 121 121 122 122 123 123 123 123 123	00000000000000000000000000000000000000) 4 4 4 4 4 4 0 4 5 6 4 5

ALIGNMENTS

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53. .409
//labbl= mature_TNF
//notel= "Tumour necrosis factor. Specifically claimed in claim 36"
                                                                                                     Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder; sparse hair; sweat gland aberration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; TNFv2; obesity-linked insulin resistance.
                                                                                  Drosophila melanogaster tumour necrosis factor variant 2 (TNFv2).
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/label=_Signal_peptide
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                 AAU77718 standard; protein; 409
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                                                             (first entry)
                                                                                                                                                                                             Drosophila melanogaster.
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RAMANATHAN C
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GUAN B.
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                                                             05-JUN-2002
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                                        AAU77718;
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Peptide
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(RAMA/)
RESULT 1
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us-09-813-329-6.rag

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The invention describes an isolated tumour necrosis factor polypeptide

(TNF). The polypeptide and polynucleotide are useful in controlling
agriculturally important pests, particularly by modifying the growth,
feeding and/or reproduction of crop-damaging insects or insects of farm
animals. The polypeptide and polynucleotide are useful for modulating
c pithalial morphogenesis, cell-matrix adhesion in flies and mammals. Thus
the polypeptide and polynucleotide may be useful for treating,
ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal
dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal
dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal
like disorders, e.g. sparse hair, abnormal or missing teeth or sweat
gland aberrations in animals (e.g. insects and potentially humans),
endotoxic shock, inflammation, haemorrhagic necrosis of tumours,
cytotoxicity and obesity-linked insulin resistance, all of which involve
TNF molecules. This is the amino acid sequence of the Drosophila
melanggaster tumour necrosis factor variant 2 protein, described in the
New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm
                                                                                                                                               Claim 6; Fig 3A-C; 119pp; English
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Sequence 409 AA;

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            Score 2162; DB 5; Length 409;
Pred. No. 7.1e-182;
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nes 409; Conservative
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Drosophila melanogaster tumour necrosis factor variant 1 (TNFv1) Ź AAU77717 standard; protein; 406 (first entry) 05-JUN-2002 AAU7711;

Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder;

53...406 /label= mature_TNF /note= "Tumour necrosis factor. Specifically claimed in endotoxic shock; inflammation; Bowen MA; Guan B, hair; sweat gland aberration; endotoxic rhagic necrosis of tumour; cytotoxicity; Xiao H, 1. .52 /label=_Signal_peptide Ramanathan CS, Location/Qualifiers obesity-linked insulin resistance 20-MAR-2001; 2001US-00813329. 21-MAR-2000; 2000US-0190816P. claim 35" Drosophila melanogaster CHEN J. RAMANATHAN C PM, Chen J, CARROLL P M. WPI; 2002-195121/25. BOWEN M A. XIAO H. GUAN B. N-PSDB; ABK11679 US2002012968-A1 haemorrhagic GUAN 31-JAN-2002 Key Peptide Carroll Protein (CARR/) BOWE/) sparse XIAO/) (RAMA/) (GUAN/) CHEN/

New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals.

Claim 6; Fig 2A-B; 119pp; English.

The invention describes an isolated tumour necrosis factor polypeptide

(TNF). The polypeptide and polynuclectide are useful in controlling
agriculturally important pests, particularly by modifying the growth,
feeding and/or reproduction of crop-damaging insects or insects of farm
animals. The polypeptide and polynuclectide are useful for modulating
cepithedial morphogenesis, cell-matrix adhesion in files and mammals. Thus
the polypeptide and polynuclectide may be useful for reating,
ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal
dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal
dysplasia-in an X-linked anhidrotic (hypohidrotic) ectodermal
dysplasia-in an X-linked anhidrotic and potentially humans),
cland aberrations in animals (e.g. insects and potentially humans),
endotoxic shock, inflammation, haemorrhagic necrosis of tumours,
cytotoxicity and obesity-linked insulin resistance, all of which involve
TNF molecules. This is the amino acid sequence of the Drosophila
melanogaster tumour necrosis factor variant 1 protein, described in the nvention

Sequence 406 AA;

ä 61 TTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDD 120 1 MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVIGFIGLGLVVAILALTIWQ 60 1 MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGFIGLGLVVAILALTIWQ 15; Length 406; Score 2082.5; DB 5; Length Pred. No. 7.3e-175; 0; Mismatches 0; Indels 96.3%; 96.4%; Conservative Similarity Best Local Simi Matches 400; Query Match Best Local S

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121 DDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGEGET 180

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Claim 6; Fig 1A-C; 119pp; English
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                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                    Sequence 409 AA;
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    note= "Tumour_necrosis factor. Specifically claimed in

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YIGNDNERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCL
                         DSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATS
                                                         KESPAPLHHRRRMHSRHRHLLVRK-----ARSEDSRPAAHFHLSSRRHQGSMGYHGDM
                                                                   ||------RMHSRHRHLLVRKGESLLSARSEDSRPAAHFHLSRRRHQGSMGYHGDM
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/label=_Signal_peptide
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                                                                                                                                                                                   AAU77716 standard; protein; 409 AA
                                                                                                                                                                                                                                                                                                     obesity-linked insulin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2001; 2001US-00813329
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        claim 34"
                                                                                                                                                                                                                                                                                                                      melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHEN J.
RAMANATHAN C S
XIAO H.
GUAN B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARROLL P M.
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N-PSDB; ABK11678.
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(XIAO/)
(GUAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOWE/)
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                                                                                                                                                                                                                                                                                                                                                               Protein
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The invention describes an isolated tumour necrosis factor polypeptide (TNF). The polypeptide and polynucleotide are useful in controlling agriculturally important pests, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating cepithalial morphogenesis, cell-matrix adresion in files and mammals. Thus the polypeptide and polynucleotide may be useful for treating, ameliorating or preventing x-linked anhidrotic (hypohidrotic) ectodermal dysplasia and x-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), endotoxic shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obesity-linked insular resistance, all of which involve TNF molecules. This is the amino acid sequence of the brosophila melanogaster tumour necrosis factor protein, described in the invention
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Pred. No. 1.5e-171;
2; Mismatches 13; Indels
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The invention describes an isolated tumour necrosis factor polypeptide (TNF). The polypeptide and polynucleotide are useful in controlling agriculturally important pests, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating controlling and polynucleotide may be useful for modulating the polypeptide and polynucleotide may be useful for reating. Thus the polypeptide and polynucleotide may be useful for reating. Thus the polypeptide and polynucleotide may be useful for reating. Thus the polypeptide and polynucleotide may be useful for reating. Thus the polypeptide and polynucleotide may be useful for reating. Thus the polypeptide and polymenting x-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), endocoxic shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obesity-linked insulin resistance, all of which involve TNF molecules. This sequence represents a tumour necrosis factor peptide contents an antigenic epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                        New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm
          endotoxic shock; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.9%; Score 149; DB 5; Length 27;
100.0%; Pred. No. 5.4e-06;
ive 0; Mismatches 0; Indels
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       sparse hair; sweat gland aberration; endotoxic haemorrhagic necrosis of tumour; cytotoxicity; obesity-linked insulin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 22; 119pp; English.
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                                                                                                                                                                               20-MAR-2001; 2001US-00813329
                                                                                                                                                                                                                21-MAR-2000; 2000US-0190816P.
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                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                                                   CHEN J.
RAMANATHAN C
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GUAN B.
                                                                                                          US2002012968-A1.
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                                                                                                                                               31-JAN-2002
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                                                                                                                                                                                                                                                                                       (RAMA/
                                                                                                                                                                                                                                                                                                                     (GUAN/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 NNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLO1840-ABLIG175) and the encoded proteins (ABB5773). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder;
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                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 29451; 21pp + Sequence Listing; English.
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Pred. No. 2.2e-137;
1; Mismatches 0;
                                                                                                       Myers EW;
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                  23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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97.8%;
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                                                                                                                                      2001-656860/75
                                                                 (PEKE ) PE CORP NY
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Best Local Similarity
                                                                                                                                                      N-PSDB; ABL11656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 325 AA;
                                                                                                                                                                                                                             interactions
                                                                                                 Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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sparse hair; sweat gland aberration; endotoxic shock; inflammation;
haemorrhagic necrosis of tumour; cytotoxicity;
obesity-linked insulin resistance.
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100.0%; Pred. No. 5.4e-06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful as an antigenic epitope
                                                                                                               20-MAR-2001; 2001US-00813329
                                                                                                                                      21-MAR-2000; 2000US-0190816P.
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168 27; Conservative
                                            Drosophila melanogaster.
                                                                                                                                                                         CHEN J.
RAMANATHAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Zis-SR protein.
                                                                                                                                                                                                                                           Chen J,
                                                                                                                                                             CARROLL P M.
                                                                                                                                                                                                                                                                  WPI; 2002-195121/25
                                                                                                                                                                                           (XIAO/) XIAO H.
(GUAN/) GUAN B.
(BOWE/) BOWEN M A.
                                                                  US2002012968-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 27 AA;
                                                                                                                                                                                                                                          Carroll PM,
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                                                                                          31-JAN-2002
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                                                                                                                                                            CARR/)
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Matches
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The invention relates to an isolated mucleic acid molecule, Zis-SR, encoding a protein involved in the secretory pathway in a cell( or its homologue or variant) or mucleic acid molecules that hybridise under high stringency condition to the Zis-SR mucleic acid. Also included are an isolated polypeptide involved in the formation of secretory granules in cells comprising the amino acid sequence spanning amino acids 243-310 of the Zis-SR protein, restoring the neuroendocrine differentiation of a cell using the nucleic acid molecule or polypeptide cited above, identifying a gene and/or protein involved in inducing regulated secretion-defective cell line under conditions that restore differentiation of the secretion-defective cell, such that secretion is restored, and the secretion-defective cell, such that secretion is restored, and the secretion-defective cell, such that secretion of the conditions cited.

Also included are modulating the secretion in a cell comprising an escretion-defective cell, such that secretion of the conditions cited.

Also included are modulating the secretion in a cell comprising an escretion of a biological activity of Zis-SR, its part or derivative in the presence of a candidate agent, where a modulator of regulated secretion is selected when the biological activity of Zis-SR, its part or derivative is measurably different in the presence of the candidate compared in its absence. The nucleic acid molecules or polypeptides are useful for regulating neuroendocrine phenotype, and for long term therapies to treat diseases or conditions associated with a loss of function, e.g. diabetes, neurodegenerative diseases such as a loss of function, e.g. diabetes, neurodegenerative diseases such as a loss of function, e.g. diabetes, conditions associated with a defect in the regulated secretory pathways in cells. The nucleic acid molecules can also be used to locate gene regions associated with genetic diseases. The present expresence conditions associated with an alloin with expressing companial sel
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1 Similarity 20.1%; Pred. No. 0.00093;
63; Conservative 60; Mismatches 130; Indels 61; Gaps
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243. .310
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ABG93245

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preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polypeptide associated with the Bax gene described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 DDVSYSSVD-DVGADYEDYTDMLN-KLNNAHTGTTPTSETTAEGEGETDSASSASNDDNV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 FDDFTSYNAHKKKQERKSRSIADVRNE---EQNIQGNHTEL---QEKSSNEATSKESPAP 246
                                                                                                                                                                                                                                                                                                         36 QLIPLV-LGFIGLGLVVAILALTIWQTTRVSHLDKEL------KSLKRVVDNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 2; human malaria parasite; vaccine; protozoacide; infection; insecticide.
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                                                                                                                                                                                                                 Length 428;
                                                                                                                                                                                                                                                             68; Mismatches 138; Indels
                                                                                                                                                                                                               6.5%; Score 141; DB 5; 0.8%; Pred. No. 0.0015;
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Matches 76; Conservative
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CARUCCI D.
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11.KEVEDKESEGEEEDEDEDLSKYKLDEDEDEDDADLSKYNLDASEEEDSNKKKSNRRSR 203
                                                                                                                                                                                                          DVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSR-PA 273
                                                                                                                                                                                                                                                   ----SSRSHRGSSSPRKRSYSSSSS----PERDRKRSRSRPSSPAVRKKRRTRSRSPE 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Baxesistant yeast or fungi, identifying, or obtaining and identifying Candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vasocropic activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions, antisense molecules and antibodies are useful as medicaments or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                     V----DGLTDEEDDDDGDGLDSIADDEDDVSYSSVDDVGADYEDYTDMLNKLNN----
                                                                                                             -----AHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. albicans BAX-associated protein fragment SEQ ID 448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG93245 standard; protein; 428 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-2000; 2000EP-00870318.
04-JAN-2001; 2001EP-00870002.
09-JAN-2001; 2001EP-00870003.
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                                                                                                                                                                                                                                                                                                    274 AHFHLSSRRRHQGS 287
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                                                                                                                  by chromosome 2 of the human malarial parasite, plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II): (I) and polyclonal antisers or a monoclonal antibody raised to imfection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. (I) (sepecially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum. Sequencing of the codenist of dentify drug resistance in P. falciparum. Sequencing of the concoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70287 and AAB18144 to AAB18352 invention, but which are not specifically mentioned within the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENAL----IDYPKKVDGLTDEE---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||: |: :: : | :| :| :| EKETEVEKKTEKDEE--GIDYEEDTDDSDKDVETEVEETDAEDKEENBEGIDDEEDKVE 624
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                                                                                                       present invention describes proteins and their fragments (I) encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 GDTPFLQCLNTVP----TNMPHKVHTCHT-----SGLIHLERNERIHLKDIHND 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     826 QGIPKEQPYNNVPYILKKGLEPKTHN-HVKEDQPNIKQGVV---KGQEPHVDDMHNN 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     773 QQYFPYXNPLEQQNYQLHH-----IIKQQQNYHPHHIIKQQQNHNPHHILQEQEKHHP
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              Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4%; Score 138.5; DB 3; Length: 20.4%; Pred. No. 0.011; tive 60; Mismatches 145; Indels
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                                                                          Disclosure; Page 60-63; 577pp; English
                              Plasmodium falciparum, useful as ant:
diagnosis of P.falciparum infection.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                             PWD,
                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                       23-MAR-2001; 2001WO-US009231
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Drosophila melanogaster.
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                                                 WO200171042-A2.
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actinic keratosis; bursitis; arteriosclerosis; artherosclerosis; hepatitis; myelofibrosis; primary thrombocythemia; psoriasis; cancer; mixed connective tissue disease; MCTD; HIV; uveitis; Crohn's disease; allergy; rheumatoid arthritis; parasitic infection.
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The present amino acid sequence is the human RNA-associated protein-8 (RNAAP-8), identified in Incyte clone 869184 derived from LUNGASTO1 library. It is expressed in reproductive, nervous, gastrointestinal and haematopoletic/fimune tissues. It has cytostatic, immunosuppressive, antinflammatory, antiarteriosclerotic, hepatotropic, keratolytic, neuroprotective, antiarterio, anti-HIV, antiallergic, antirheumatic, virucide, antiarthritic, opthalmological and antimicrobial activity. RNAAP antibodies are useful for diagnosis of diseases associated with proliferative, autoimmune, inflammatory and infectious disorders, inclinic keratosis, bursitis, arteriosclerosis, artherosclerosis, cirhosis, hepatitis, myelofibrosis, mixed connective tissue disease, cirhosis, hepatitis, myelofibrosis, mixed connective tissue disease, contrantial, primary thrombocythemia and cancer, HIV, allergies, containts, inferiors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 KRVVD----NLQQRLG-----INYLD-----EFDEFQKEYENALIDYPKKVDG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 ---LTDEEDDDGGGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                  Human RNA-associated proteins useful in diagnosing, treating and preventing cell proliferative, autoimmune, inflammatory and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 FARRISCNRCGREKTTEAKMMKAGGTEIGKTLAEKSRGLFSANDWQCKTCSNVNWARRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 FPAKATSTATAQRRTRQLIPLVLGFIGLGLVVA----ILALTIWQTTRVSHLDKELKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARS----EDSRPAAHFHLSSRRRHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTEL
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                                                                                                                                                                  GA;
                                                                                                                                                                    Gorgone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches 107; Indels
                                                                                                                                                                ue H, Tang YT, Corley NC, Guegler KJ,
Baughn MR, Lal P, Bandman O, Reddy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 ----EDEDEDDADLSKYN----LDASEEEDSNKKKSNRRSRS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 PASILKEVEDKESEGEE---EDEDEDLSKYKLD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%; Score 137; DB 3; 21.2%; Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 85-86; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
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                                                99WO-US019361
                                                                                98US-0097550P
99US-0115639P
                                                                                                                                                                                   Patterson C, Baughn MR, Shih LL, Yang J, Lu DAM;
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                                                                                                                                 (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parasitic infections
                                                                                                                                                                                                                                   WPI: 2000-237651/20
                                                                                                                                                                  Yue H,
                                                                                                                                                                                                                                                  N-PSDB; AAZ51257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 330 AA;
                                                20-AUG-1999;
                                                                                21-AUG-1998
               02-MAR-2000
                                                                                                                                                                  Hillman JL,
                                                                                                                                                                                                                                                                                                                   disorders.
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ABB67173
ID ABB67
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ABB67173 standard; protein; 532 AA

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interactions
                                                             26-MAR-2002
                                                                                                                        Drosophila;
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                              ABB65698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEEDDDDGDGLDSIADDEDDDVSYSSVDD-----VGADYEDYTDMLNKLNNA-----HTG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NVFDDF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 DSYNPNEGRGSRRRPGAA---RPSSNRQINGHSSKRRLNKSPANAAPGPSLPRRTRRIA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEEDDDD------DDDDDDDEEEASTRGRSRRRNGVAVSASSSGSNRVTSSSAAQQRRG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 KSSSSEEEEEETSAQATSDASSDEEERAQSNDSSPQQTRTRRARQRQRLSDDSNINDSE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RMHSRH-----RHLLVRKARSEDSR------PAAHFHLSSRRRHQGS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSSAEEAASHSQHDESTQDSQIGRRKGRSASSRSIGNGPSTSAAAAANSSLESPSRNTRA 381
                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 28311; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%; Score 137; DB 4; Length 532; 22.6%; Pred. No. 0.0046; ive 37; Mismatches 93; Indels
                                                            Drosophila melanogaster polypeptide SEQ ID NO 28311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :: |: | | | :: |: | | NGTRTSSHLGAEND-HSY--HLPVRNGRIIESDT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGYHGDMYIGNDNERNSYQGHFQTRDGVLTVTNT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTPTSETTAEGEGETDSASSASNDD------
                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                             PWD,
                                                                                                                                                                                                                                  2001WO-US009231
                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Conservative
                                                                                                                                                                                                                                                                                                                                             댜
                                                                                                                                       Drosophila melanogaster
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                                                                                                                                                                    WO200171042-A2
                                                                                                         pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                        interactions.
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                             26-MAR-2002
                                                                                                                                                                                                   27-SEP-2001
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ABB67173;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7137-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNE---
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                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 23886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.3%; Score 137; DB 4; L
11.8%; Pred. No. 0.035;
ve 45; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EW;
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ABB65698 standard; protein; 2175 AA.
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11-JUL-2000; 2000US-00614150
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les 64; Conservative
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                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
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N-PSDB; ABL09801
                                                                                                                                                                                                                                                                                   pharmaceutical
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08-SEP-2000; 208-SEP-2000; 208-SEP-2000; 214-SEP-2000; 214-SEP-2000; 214-SEP-2000; 214-SEP-2000; 214-SEP-2000; 221-SEP-2000; 221
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02-0CT-2000)
02-0CT-2000)
02-0CT-2000)
13-0CT-2000)
13-0CT-2000)
20-0CT-2000)
20-0CT-2000)
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20-OCT-2000;

08-NOV-2000;

09-NOV-2000;

17-NOV-2000;

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17-NOV-2000;
17-NOV-2000;
  Human, neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
                                                                                                                                                                                                Novel human neoplastic disease associated polypeptide #261
                                                           AAU21828 standard; protein; 330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0199874P

2000US-0190076P

2000US-019121P

2000US-0191318P

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2000US-0249265P.
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01-SEP-2000; 2000US-0229344P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention sequences encoding for these polypeptides. The sequences of the invention disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as hyperproliferative disorders (alsorders, pandult liver cancer, childhood cerebellar astrocytoma, or hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders, reproductive disorders, jamune system disorders, muscular disorders, reproductive disorders and renal disorders. The polymucleotide sequences of the invention are also useful in gene therapy. AM011568-AM01361 represent the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 KRVVD-----NLQQRLG-----INYLD-----EFDEFQKEYENALIDYPKKVDG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 CNMCNTPKYAKLEERTGYGGGFNERENVEYIEREESDGEYDEFGRKKKK----YRGKAVG 150
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48; Mismatches 108; Indels
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17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0249300P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251999P.
08-DEC-2000; 2000US-0251999P.
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autoimmune disease; human immundeficiency virus; HUY; infection; ananamia, rheumatoid arthritis, multiple sclerosis; cancer; melanoma; hyperproliferative disorder; neurological disease; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cerebrovascular disorder; angina; ocular disorder; corneal infection; wound healing; biorhythm transplantation; mesodermal tissue differentiation; embryonic stem cell; catabolism; anabolism; energy storage; mental state; hormone; appetite; reproductive potential; memory; stress; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted DNA repair and processing protein; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                    Human DNA repair and processing protein, SEQ ID No 34.
                                                                                                                                                                                              AAU86946 standard; protein; 330 AA
286 GSMGYHGDMYIGNDN--ERN 303
                                                    GSSSPRKRSYSSSSSSPERN 294
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2000US-0229343P.
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2000US-0229513P.
2000US-0230437P.
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27-SEP-2000;
29-SEP-2000;
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The invention relates to novel isolated nucleic acid molecules (I)
encoding human secreted DNA repair and processing proteins (II). (I) and
encoding human secreted DNA repair and processing proteins (II). (I) and
(II) are used to prevent, treat or ameliorate a medicial condition e.g. in
humans. (I) and (II) may be used in the prevention, treatment and
eiganosis of diseases associated with inappropriate expression of (II),
cereased expression of (II) by rectifying mutations or deletions in a
decreased expression of (II) by rectifying mutations or deletions in a
patient's genome that affect the activity of (II). (I) and complementary
cerease chain reactions (PCR) to detect and quantitate the presence
C patients and also be used as DNA probes in diagnostic assays (e.g.
co journaliar sequences in samples, and so which patients may be in need of
crestorative therapy. (II) may also be used as antigens in the production
of antibodies and in assays to identify modulators (agonists and
antibodies and antagonists may also be used to down regulate expression
and activity of (II). The anti-(II) antibodies may also be used as
disorders include e.g. immune/autoimmune diseases (e.g. human
cc and multiple sclerosis, cancers and hyperproliferative disorders (e.g.
mulmondeficiency virus (HIV), infections, anaemia, rheumatoid arthritis
cmelanomas), neurological diseases (e.g. Alzheimer's disease and
carrest, angina and thrombosis), infections caused by bacteria, viruses
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21.2%; Pred. No. 0.0035;
Live 48; Mismatches 108; Indels 96; Gaps 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding human secreted DNA repair and processing proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
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2000US-0249218P-
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N-PSDB; ABK43159.
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Best Local Similarity
Matches 68; Conserv
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05-DEC-2000;
06-DEC-2000;
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17-NOV-2000;

Search completed: September 13, 2004, 10:34:22 Job time : 62 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-08-431-080-28
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US-08-33-152A-29
US-08-130-152A-29
US-08-007-999B-4
US-08-99-114-3
US-08-99-114-3
US-09-201-313-3
US-07-712-476A-1
US-09-134-253-1
US-09-105-343A-5
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US-09-105-343A-5
US-09-105-343A-5
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US-09-105-343A-4
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US-08-568-459A-4
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                                                                                                                                                                                                                                                                                                                                                                                               389414 seqs, 51625971 residues
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 NAHTGTTPTSETTAE--------GEGGETDSASSASNDDNVFDDF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 DGSDSDSB-----TSSDDENIDFVKLTAQRKKRAMKALSAMNTNSNTLYSSRENSNK 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 ISFGNGNEGYNEDIGEEVLDLKNKENNGNEEDKLDSKVMLGNNDELRFPNISESDESE- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 APLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGY-----HGDMYIGND 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 ------YDIDQDAYPDVINNEDSHGEIGTDLETGEDDLPILEE 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 129; DB 1; Length 1085;
19.9%; Pred. No. 0.0039;
Live 48; Mismatches 126; Indels 120; Gaps
                                                     ZITO
ZITO
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,080
FILING DATE: CONCURRENTLY Herewith
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELEPHONE: (512) 418-3000
TELEFRAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGLDSIADDEDDDVSYSSVDDVGADYED----
                                                   UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 19.99
Matches 73; Conservative
P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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                                                  COUNTRY:
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US-08-938-534-28
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Sequence 28, Application US/08938534 Patent No. 2916752 GENERAL INFORMATION: APPLICANT: Gottschling, Daniel E.

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69 KELKSLKRVVDNLQQRLGINYLDEFDEFQ-----KEYENALIDYPKKVDGLTDEEDDDDG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGLDSIADDEDDDVSYSSVDDVGADYED------YTDMLNKLN 160
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APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/938,534
FILING DATE: 26-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMULICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                           STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAC
                                                                                                                                                                    STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: OCCODER 20, 1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDIPFLQ 352
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US-08-938-534-28
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36,688
ER: 0609.4120000
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TELECOMMUNICATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-371-2540
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346 GDTPFLQ 352
                                   417 FÜMPFYE 423
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US-08-339-152A-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 TSY-NAHKKKQERKSRSIADVRNEEQN------IQGNHTELQEKSSNEATSKESP 244
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                               Sequence 28, Application US/09345294
Patent No. 6387619
GENERAL INFORMATION:
APPLICANT: Gottschling, Daniel E.
Singer, Mitham S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ANDRESS:
ADDRESSE ANDOIG, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                  COUNTEY: UNITED STATES OF AMERICA

ZIP: 77210

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEACATION PC-DOS/NS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,294

FILING DATE: 30-Jun-1999
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: «Unknown»

ATTORNEY/AGENT INFORMATION:
NAME: PARKEr, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEFAK: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 28:
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SEQUENCE DESCRIPTION: SEQ ID NO: 28:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                US-09-345-294-28
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275 YYDTFK--GDDYNEE----NPTEPGSDGTMSDKEITHDVKVPPTPLPTNDVDVYFETSAD 328
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Patent No. 5643726
GENERAL INFORMATION:
APPLICANT: Ranzi, Rudolph E.
APPLICANT: Kovacs, Dora M.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
Annuescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 -RRMHS-RH-RHLLV---RKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERN 303
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                                                                                                                                                                                                                                                              ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Ave., NW, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILLING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTOREX/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
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Sequence 4, Application US/08689276A
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                                                                                                                                                                                                                                                                   STREET:
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                                       Patent No.
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APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzi, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne ...
STEPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 5.7%; Score 122.5; DB 2; Length 706; 1 Similarity 21.1%; Pred. No. 0.0084; 63; Conservative 36; Mismatches 105; Indels 95
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                                                                                                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,999B
FILING DATE: 21-AN-1993
PRIOR APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
FRICK APPLICATION NUMBER: US 07/872,642
FILING DATE: 10-ANG-1992
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-ANG-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 0609:3520002/JAG/GKT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)311-2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 DNVFDDFTS----YNAHKKKQER-----
   Sequence 4, Application US/08007999B
Patent No. 5851787
GENERAL INFORMATION:
APPLICANT: Wasco, Wilma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 706 amino acids
amino acid
                                                                                                                                                                                                                                                                         CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 63; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-007-999B-4
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US-08-689-276A-4

13; 275 YYDTEK--GDDYNEE----NPTEPGSDGTMSDKEITHDVKVPPTPLPTNDVDVYFETSAD 328 91 DEFDEFQKEYENALIDY-----PKKVD-----GLTDEEDDDDGDGLDSIADDEDDDV 137 138 SYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGE-----GETDSASSASND 189 251 -RRMHS-RH-RHLLV---RKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERN 303 Gaps 95; GENERAL INFORMATION:
APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Tanzi, Rudolph
APPLICANT: Tanzi, Rudolph
APPLICANT: Tanzi, Rudolph
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. DB 2; Length 706; 213 IADVRNEEONIQGNHTELQEKSSNE-----ATSKESPAPLHHR SSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. T: 1100 New York Ave., NW Washington CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME:

NAME:

ACOLDSTEIN

REGISTRATION NUMBER:

APPLICATION NUMBER:

ATTORNEY/AGENT NUMBER:

APPLICATION NUMBER:

ATTORNEY/AGENT NUM 190 DNVFDDFTS-----YNAHKKKQER------MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS TELEFAX: (202)371-2540 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: (202) 371-2571 706 amino acids amino acid TOPOLOGY: linear MOLECULE TYPE: protein ZIP: 20005 COMPUTER READABLE FORM: ò

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98 KEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLN 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 LLVRKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERNS-----YQGHFQTR 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 --KSRSIADVRNEEQNIQGNHTELQEKSSNEATSKE-----SPAPLHHRRRMHSRHRH 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 122.5; DB 4; ilarity 20.0%; Pred. No. 0.0086; Conservative 40; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                             HUMAN NUCLEOLIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diakette
COMPUTER: Diakette
COMPUTER: Diakette
COMPUTER: BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,333
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/990,114
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAMAF: PILING DATE:
NAMAF: PILING DATE: PILING DATE:
NAMAF: PILING DATE: PILIN
                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Yue, Henry
APPLICANT: Corlay, Neil C.
APPLICANT: Shah, Purvi
ITILE OF INVENTION: HUMAN NUCLEOLIN-LIKE PR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0451 US
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 650-855-0555
336 DLAVVDVRTGTNRKFGYVDFESAED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 DGVLTVTNTGLYYVYAQICYNNSHD 337
                                                                                                                                                  // Sequence 3, Application US/09241333
// Patent No. 6313266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 714 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
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Best Local Similarity
Matches 53; Conserva
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LIBRARY: GenBank
CLONE: 128842
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                                                                                                                        US-09-241-333-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 KLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNA------HKKKQER-- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 PVVKGKQĠKVAAAAPASĖDĖDĖEEDEEEEEDEEEEDDSEEERAMEITPAKGKKAPAKVV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 --KSRSIADVRNEEQNIQGNHTELQEKSSNEATSKE-----SPAPLHHRRRMHSRHRH 259
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                                                                                                                                                                                                          APPLICANT: Bandman, Olga
APPLICANT: Yue, Hanry
APPLICANT: Orley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
TUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 122.5; DB 2;
20.0%; Pred. No. 0.0086;
tive 40; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESD for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,114
                                                                                                                                                                                                                                                                                                                                                            STREET: JOYCE Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy 3, 79
REGISTRATION NUMBER: 36, 749
REPERENCE/DOCKET NUMBER: 9F-0451 US
TELECOMMUNICATION:
TELEFAX: 650-855-0555
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                                                                                                              Sequence 3, Application US/08990114
Patent No. 5932475
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 anino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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CLONE: 128842
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                                                                                 US-08-990-114-3
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63;

Length 714; Indele ø

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; ORGANISM: Homo sapiens
US-09-134-253-1
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ORGANISM: Homo sapiens
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 NAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRH 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 ETHSHKQSRLYKRKA---NDESN---BHSDVIDSQELSKVSRE----FHSHEFHS-HED 265
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22.8%; Pred. No. 0.003;
tive 30; Mismatches 78; Indels 99;
                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
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MLVVDPKSKEEDK-----HLKFRISHE 287
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PS/2

COMPUTER: IBM PS/2

SOFTWARE: WORDPRERECT 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/712,476A
FILING DATE: 19910610
CLASSIFICATION DATA:
APPLICATION NUMBER: TOWN OFFICE FILING DATE:
FILING DATE: TOWN OFFICE FILING DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SUZAMB E. MILLET
REGISTRATION NUMBER: 32,279
REGISTRATION NUMBER: 32,279
REGISTRATION NUMBER: UPN 0473
TELECOMMUNICATION:
MOTORIAND NUMBER: UPN 0473
TELECOMMUNICATION:
MOTORIAND NUMBER: UPN 0473
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336 DLAVVDVRIGINRKFGYVDFESAED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215) 568 3100
TELEFAX: (215) 568 3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
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AMINO ACID
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Best Local Similarity
Matches 61; Conserva
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                                                                      US-07-712-476A-1
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RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 EETNDFKQE-----TLPSKSNESHDHMDDMDDEDDDDHVDSQDSIDSNDSDDTDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 PDIQYPDATDEDITSHMESEELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQLDD-QSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 ETHSHKQSRLYKRKA---NDESN---EHSDVIDSQELSKVSRE-----FHSHEFHS-HED
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Sequence 1, Application US/09134253
Fatent NO. 6509026
GENERAL INFORMATION:
TITLE OF INVENTION: Osteopontin Coated Surfaces and Methods of Use
TITLE REPERENCE: cme-100cp
CURRENT APPLICATION NUMBER: US/09/134,253
CURRENT PILING DATE: 1998-08-14
EARLIER FILING DATE: 1998-08-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 314
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Sequence 2, Application US/09206576

GENERAL INFORMATION:
APPLICANT: Glachelli, Cecilia M.
APPLICANT: Steitz, Susie
TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification
FITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification
FILE REFERENCE: P-UW 3244
CURRENT FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Datentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
5.6%; Score 121.5; DB 4;
Best Local Similarity 22.8%; Pred. No. 0.0032;
Matches 61; Conservative 30; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.6%; Score 121.5; DB 4;
22.8%; Pred. No. 0.0032;
Live 30; Mismatches 78;
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284 MLVVDPKSKEEDK-----HLKFRISHE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 LLV--RKARSEDSRPAAHFHLSSRRHQ 285
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203 KKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLV 262
                                                                             103 ARRA-----IAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVT 156
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DIAGNOSIS OF DISEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
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OPERATING SYSTEM: Windows
OPETWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
EREPRENCE/DOCKET NUMBER: 6048.US.P2
TELECOMMUNICATION INPORMATION:
TELEDHONE: 847-935-1729
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09105343A
Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
TITLE OF INVENTION: MEMBER OF THE TNF
TITLE OF INVENTION: FOR TREATMENT AND
                                                                                                                                                                  263 -- RKARSEDSRPAAHFHLSSRRHQ 285
                                                                                                                                                                                                           255 VDPKSKEEDK-----HLKFRISHE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/09/105,343A
12-FEB-1998
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
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COUNTRY: USA
ZIP: 60064-6050
COMMUTER READABLE FORM:
MEDIUM TYPE: Diskette
"""TER: IBM Compatible
"""TER: IBM Compatible
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TYPE: amino acid
STRANDEDNESS: single
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TELEX:
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LENGTH: 249 amino acid
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                                                                                                                                                                                                                                                                                                                                                         US-09-105-343A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-105-343A-2
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                                                                                                                          177 PDIQYPDATDEDITSHMESEELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQLDD-QSA 235
                                                                                                                                                                                                                                      236 ETHSHKQSRLYKRKA---NDESN---EHSDVIDSQELSKVSRE----FHSHEFHS-HED 283
118 HQSDESHHSDESDELVTDFPTDLPATEVFTPVVPTVD-TYDGRGDSVVYGLRSKSKKFRR 176
                                                                   DSASSASNDDNVFDDFTSY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 DEPOKEYENALIDYPKK-----SYSS 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------DSASSASNDDNVFDDFTSYNAH 202
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                                                                                                                                                                                          200 NAHKKKOERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRH
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ZIF: 19103

CONSUTER READMBLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2

OPERATING SYSTEM: PC DOS
SOFTWARE: WORDPERFECT 5.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/712,476A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5304496ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/07712476A
Patent No. 5304496
GENERAL INFORMATION:
APPLICANT: Hoyer et al.
TITLE OF INVENTION: Biological Regulation of TITLE OF INVENTION: Biological Regulation of WINGER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       LLV--RKARSEDSRPAAHFHLSSRRHQ 285
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REGISTRATION NUMBER: 32,279
REFRENCE/DOCKET NUMBER: UPN (TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568 3100
INFORMATION FOR SEQ 1D NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Suzanne E. Miller
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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US-07-712-476A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 HKQSRLYKRKA---NDESN---EHSDVIDSQELSKVSRE----FHSHEFHS-HEDMLVV 273
                                                                                                                                                                                                                                                                                                                                                                                                                       41 VLGFIGLGLVVAILALTIWQTTRVSHLDKELKSLKRVVDNLQQRLGINYLDEF-----D 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VICFCLIGITCAL---PVKQADSGSSEEKQLYN-------KYPDAVATWLNPD 47
                                                                                                                                                                                                                                                                                                                                         Query Match 5.4%; Score 116; DB 6; Length 300;
Best Local Similarity 23.1%; Pred. No. 0.0099;
Matches 75; Conservative 32; Mismatches 101; Indels 116; Gaps
                                                    RESULT 15
5340934-6
; PACENT NO. 5340934
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; UNRERN APPLICATION DATA:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO: 6:
; LENGTH: 300
212 VSGLLALRPGSSLRIRTL---PWAHLKAAPFLTYFGLFQV 248
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Search completed: September 13, 2004, 10:36:16 Job time : 20 secs us-09-813-329-6.rapb

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(without alignments)
1001.237 Million cell updates/sec
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1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409
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// Ggn2_6/ptodata/2/pubpa/PCT_NEW_PUB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/DGCO/BUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/PCTUG/BUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/PCTUG/BUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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// Ggn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO9_BUBCOMB.pep:*
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// Ggn2_6/ptodata/2/pubpaa/USO9_BUBCOMB.pep:*
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// Ggn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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// Ggn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	144,144	rescriberon	Sequence 6, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 54, Appl	Sequence 64, Appl	Sequence 148275,	Sequence 448, App	Sequence 154595,	Sequence 434, App	Sequence 34, Appl	Sequence 34, Appl	Sequence 555, App	Sequence 34, Appl	Sequence 8, Appli	Sequence 2, Appli
SUMMARIES	4		US-09-813-329-6	US-09-813-329-4	US-09-813-329-2	US-09-813-329-54	US-09-813-329-64	US-10-437-963-148275	US-10-451-467A-448	US-10-437-963-154595	US-10-408-765A-434	US-09-764-848-34	US-10-116-016-34	US-10-103-313-555	US-10-222-020-34	US-09-813-329-8	US-09-729-658B-2
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Sequence 42, Appl Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 250021, Sequence 13752, Sequence 13752, Sequence 18876, Sequence 12955, Appli Sequence 12955, Appli Sequence 12955, Appli Sequence 125345, Sequence 13837, Appli Sequence 176, Appli Sequence 176, Appli Sequence 177, Appli Sequence 147, Appli Sequence 147, Appli Sequence 147, Appli	Sequence 1, Applia Sequence 227, App Sequence 172, App Sequence 303, App Sequence 336, App
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391 391 391 167 891 167 872 1111 17374 173	311444 31444
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ALIGNMENTS

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Sequence 6, Application US/09813329

Patent No. US2002012968A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Molec
TITLE OF INVENTION: Variants Thereof
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Version 3.0

SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGEGET 180
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100.0%; Score 2162; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 4.1e-167;
Matches 409; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Drosophila melanogastor
US-09-813-329-6
                                                                                                                                                                                                                                                                                                                                                                                                                      409
JS-09-813-329-6
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Gaps .; 0 9 9 180 180 240 300 300 360 360

Length 27;

DB 9;

Score 149;

6.9%;

Query Match

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Suibb Company

APPLICANT: Bristol-Myers Suibb Company

TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class MolecTITLE OF INVENTION: Variants Thereof

FILE REFERENCE: D0016.np

CURRENT APPLICATION NUMBER: US/09/813,329

CURRENT PILING DATE: 2001-03-20

PRIOR APPLICATION NUMBER: 60/190,816

PRIOR FILING DATE: 2000-03-21

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Version 3.0

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54, Application US/09813329
Patent No. US20020012968A1
GENERAL INFORMATION:
APPLICANT: Bristcl-Myers Sulbb Company
TITLE OF INVENTION: Variants Thereof
FITLE OF INVENTION: Variants Thereof
FITLE SEFERENCE: D0016, np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT APPLICATION NUMBER: 60/190,816
PRIOR PILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE PATENTIAL VERSION 3.0
SEQ ID NO 54
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                           TTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDD 120
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                                                                                                                                                                                                                                                                                                               Length 409;
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 96.3%; Pred. No. 1.3e-157;
Matches 394; Conservative 2; Mismarches 10
                                                                                                                                                                                                                                         TYPE: PRT CORGANISM: Drosophila melanogastor US-09-813-329-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-54
                                                                                                                                                                                                                           LENGTH: 409
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Retent No. US20020012968A1

Retent No. US20020012968A1

APPLICANT: Bristol-Myers Suibb Company

TITLE OF INVENTION: Variants Thereof

FILE OF INVENTION: Variants Thereof

FILE REPERENCE: D0016.np

CURRENT FILING DATE: 2001-03-20

RIOR APPLICATION NUMBER: 6/190,816

PRIOR PILING DATE: 2000-03-21

NUMBER: OF SEQ ID NGS: 65

SPOTWARR: Patentin version 3.0

SEQ ID NO 4
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ERNSYQCHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQCDTPFLQCLNTVPTN
                                                                                                                                          KESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDN
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Pred. No. 1.2e-160;
0; Mismatches 0; Indels 15;
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; Sequence 2, Application US/09813329
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Best Local Similarity 96.4%;
Matches 400; Conservative
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APPLICANT: CONTREAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: EBERHARDT, INES
APPLICANT: BERHARDT, INES
APPLICANT: BERHARDT, INES
APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKGANS, REKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
FILLE OF INVENTION: VEAST AND FUNCI
FILLE OF INVENTION NUMBER: BY 00870318.3
PRIOR FILLING DATE: 2000-12-2
PRIOR FILLING DATE: 2001-01-04
PRIOR FILLING DATE: 2001-01-04
PRIOR FILLING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PATENTION VERSION 3.1
SOFTWARE: PATENTION VERSION 3.1
                                                                                                                                                                                                                                  : :| : ::: ||: ::: | 273 KSKRRGRSSRRKKRSKQSD 332
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                                                                                                                                     220 EQNIQGNHTELQEKSSNE------ATSKESPAPLHHRRRMHSRHRHLLVRKAR 266
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              108 PKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTT 167
                                         247 LHHRRRMHSR--HRHLLVRKARSE-----DSRPAA-----HFHLSSRRR- 283
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; Pred. No. 0.0063;
68; Mismatches 138; Indels 84; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 20.8%;
Matches 76; Conservative 6
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Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brobazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 148275

LENGTH: 511
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class Mole TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class Mole TITLE OF INVENTION: Variants Thereof TITLE OF INVENTION: Variants Thereof CURENT APPLICATION NUMBER: US/09/813,329 CURRENT APPLICATION NUMBER: 60/190,816 PRIOR FILING DATE: 2000-03-21 NUMBER OF SEQ ID NOS: 65 SOFTWARE: Patentin version 3.0 SEQ ID NO 64
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23.5%; Pred. No. 0.0035;
tive 49; Mismatches 85; Indels 55;
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US-10-437-963-148275
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Local Similarity 100.0%; Pred. No. 3.5e-05;
ieb 27; Conservative 0; Mismatches 0;
            Pred. No. 3.5e-05;
100.0%; Preu. ...
                                                                              311 TRDGVLTVTNTGLYYVYAQICYNNSHD 337
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                                                                                                         1 TRDGVLTVTNTGLYYVYAQICYNNSHD 27
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; Patent No. US20020012968A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-64
            Best Local Similarity 100.
Matches 27; Conservative
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ORGANISM: Oryza sativa
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US-09-813-329-64
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Best Local S:
Matches 58
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                                                                                                                                                                                                                                                                                       DVSYSSVDDVGADYEDYTDMLNKLNNAHTG-TTPTSETTAEGEGETDSA---SSASNDDN 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 POHVHHGLVDEEEEEEITVQFGHYVASHQPRGHKSDEEDFQDEYKTEVPHHHHRVPRE 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 KRVVD-----NLQQRLG-----INYLD-----EFDEFQKEYENALIDYPKKVDG 113
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                                                                                                                                                                        ----GLDSIADDEDD
                                                                                                               Gaps
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                                                  Length 699;
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Patent No. US20020077270A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ08
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-77
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 53
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21.2%; Pred. No. 0.014;
tive 48; Mismatches 108; Indels
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6.3%; Score 137; DB 16;
Best Local Similarity 20.7%; Pred. No. 0.026;
Matches 60; Conservative 38; Mismatches 116;
                                                                                                                                                                    91 DEFDEFOKEYENALIDYPKKVD---GLTDEEDDDDGD
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SEQ ID NO 34
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Best Local Similarity
Matches 68; Conserv
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TYPE: PRT
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                                                                                                                     RESULT 8
US-10-437-963-154595
US-10-437-963-154595
Sequence 154595, Application US/10437963
Sequence 154595, Application US/10437963
Sequence 154595, Application US/10437963
Sequence 154595, Application No. US20040123343A1
Septicant: La Rosa, Thomas J.
APPLICANT: Expurity May Wei
APPLICANT: Cao, Yongwei
APPLICANT: Boucharov, Andrey A.
APPLICANT: Bucharov, Andrey A.
APPLICANT: Bucharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 30-215321)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 154595
LEGTH: 406
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| Sequence 434, Application US/10408765A
| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Ghosh, Soumitra S. APPLICANT: Tahay, Boin D. APPLICANT: Tahay, Boin G. APPLICANT: Taylor, Steven W. APPLICANT: Gloson, Bradford W. APPLICANT: Gloson, Stopen W. APPLICANT: Gloson, Stopen W. APPLICANT: Gloson, Saven W. APPLICANT: Gloson, Bradford W. APPLICANT: Gloson, Stopen W. APPLICANT: Gloson, Glo
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US-10-437-963-154595
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; ORGANISM: Homo sapiens
US-10-408-765A-434
   319 TNTGLY 324
                                                         420 A-SGSY 424
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ORGANISM: Homo sapiens
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Best Local
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NAME/KEY: misc feature
LOCATION: (179)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 555, Application US/10103313

Publication No. US20030082758A1

GENERAL INFORMATION:

TAPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ07C1

CURRENT APPLICATION NUMBER: US/10/103,313

CURRENT FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 653

Prior Application removed - See File Wrapper or Palm

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 555

LENGTH: 330
                                                                                                                       Sequence 34, Application US/10116016; Publication No. US20030054379A1; GENERAL INPORMATION:

APPLICANT: Soean et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PT208C1.

CURRENT APPLICATION NUMBER: US/10/116,016;

CURRENT FILING DATE: 2002-04-05; Prior Application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 53; SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 34
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                                 275 GSSSPRKRSYSSSSSSPERN 294
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Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-10-116-016-34
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 330
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114 ---LTDEEDDDDGDGLDSIADDEDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
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TILE REPERENCE: PT208C3

CURRENT APPLICATION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PT208C3

CURRENT APPLICATION NUMBER: US/10/222,020

CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 10/116,016

PRIOR APPLICATION NUMBER: 09/764,848

PRIOR APPLICATION NUMBER: 09/764,848

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR PILING DATE: 2000-01-31

PRIOR PLING DATE: 2000-02-04

PRIOR PLING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR PLING DATE: 2000-03-04

PRIOR PLING DATE: 2000-06-28

PRIOR PELICATION NUMBER: 60/227,788

PRIOR PLING DATE: 2000-06-14

PRIOR PLING DATE: 2000-06-14

PRIOR PLING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR APPLICATION NUMBER: 60/227,768

PRIOR APPLICATION NUMBER: 60/227,768
                                                                                                                                                                                                           6.2%; Score 135; DB 14; Length 330; 21.2%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                    48; Mismatches 108; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICATION NUMBER: 60/218,290
ING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/226,868
FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/225,447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/216,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34, Application US/10222020 Publication No. US20030175739A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 GSSSPRKRSYSSSSSSPERN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      000-08-14
                                                                                                                                                                                                                                                                                    Conservative
FEATURE:

NAMEKEY: misc feature

LOCATION: (179)

OTHER INFERMATION: Xaa
US-10-103-313-555
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                    68;
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PRIOR APPLICATION NUMBER: 60/215,267
PRIOR APPLICATION NUMBER: 60/216,880
PRIOR FILING DATE: 2000-09-14
PRIOR PALLICATION NUMBER: 60/216,880
PRIOR PALLICATION NUMBER: 60/216,880
PRIOR PAPLICATION NUMBER: 60/211,669
PRIOR PAPLICATION NUMBER: 60/211,669
PRIOR PAPLICATION NUMBER: 60/214,274
PRIOR PAPLICATION NUMBER: 60/214,274
PRIOR PAPLICATION NUMBER: 60/214,223
PRIOR PAPLICATION NUMBER: 60/214,223
PRIOR PAPLICATION NUMBER: 60/214,223
PRIOR PAPLICATION NUMBER: 60/214,128
PRIOR PAPLICATION NUMBER: 60/214,128
PRIOR PAPLICATION NUMBER: 60/214,128
PRIOR APPLICATION NUMBER: 60/214,139
PRIOR APPLICATION NUMBER: 60/214,139
PRIOR APPLICATION NUMBER: 60/214,139
PRIOR APPLICATION NUMBER: 60/214,139
PRIOR PAPLICATION NUMBER: 60/229,344
PRIOR PAPLICATION NUMBER: 60/229,344
PRIOR PAPLICATION NUMBER: 60/229,345
PRIOR PAPLICATION NUMBER: 60/229,339
PRIOR PAPLICATION NUMBER: 60/239,339
PRIOR PAPLICATION

PRIOR APPLICATION NUMBER: 60/249,935
PRIOR PLICATION NUMBER: 60/239,935
PRIOR FILING DATE: 2000-10-20
PRIOR PLICATION NUMBER: 60/249,337
PRIOR FILING DATE: 2000-11-3
PRIOR PLICATION NUMBER: 60/246,474
PRIOR PLILING DATE: 2000-11-00
PRIOR PLILING DATE: 2000-11-00
PRIOR PLILING DATE: 2000-11-00
PRIOR PLILING DATE: 2000-11-00
PRIOR PLILING DATE: 2000-11-01
PRIOR PLILING DATE: 2000-01-12
PRIOR PLILING DATE: 2000-01-12
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PRIOR PLILING DATE: 2000-01-12
PRIOR PLILING DATE: 2000-01-13
PRIOR PLILING DATE: 2000-01-14
PRIOR PLILING DATE: 2000-01-17
PRIOR PLILING DATE: 2000-01-17
PRIOR PLILING DATE: 2000-11-17
PRIOR PLILING DATE: 2000-01-17
PRIOR PLILING DA

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APPLICANT: Zonana et al.
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REPERENCE: 55924
FILE REPERENCE: 55924
CURRENT APPLICATION NUMBER: US/09/729,658B
CURRENT FILING DATE: 2000-12-04
FRIOR APPLICATION NUMBER: 60/092,279
FRIOR PILING DATE: 1999-06-29
FRIOR PILING DATE: 1998-07-09
FRIOR PILING DATE: 1998-12-15
FRIOR FILING DATE: 199
                                                                                                                                                                                                                     295 VLVDGTYFIXSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTN-YNTCYTAGVCL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 KARSEDSRPAAHFHLSSRRRHQGS-MGYHGDMYIG--NDNER---NSYQGHFQTRDGVLT 317
                   264 KARSEDSRPAAHFHLSSRRHQGS-MGYHGDMYIG--NDNER---NSYQGHFQTRDGVLT 317
                                                                                                                                                                  318 VINIGLYYVYAQ -- ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 VINTGLYYVYAQ--ICYNNSHDQNGFIVFQGDTPFLQCLNTVPINMPHKVHTCHTSGLIH 375
                                                                   240 KAGTRENQPAV-VHLQG----QGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 VLVDGTYFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTN-YNTCYTAGVCL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 132; DB 10;
Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                   |: ::| :| : | : ::| | 354 LKARQKIAVKMVHADIS--INMSKHTTFFGAIRL 385
                                                                                                                                                                                                                                                                                                                        376 LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.1%; Score 132; DB Best Local Similarity 28.6%; Pred. No. 0.03; Matches 44; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 13, 2004, 10:46:53 Job time : 133 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09729658B; Publication No. US20030023991A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-729-658B-2
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: Vo. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Vo. US20020013968A1el Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Vo. US2002001393329
FILE REFERENCE: D0016.np
CURRENT APPLICATION UNMER: US/09/813,329
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR APPLICATION NUMBER: 60/190,816
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 CNMCNTPKYAKLEERTGYGGFNERENVEYIEREESDGEYDEFGRKKKK----YRGKAVG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 ---LTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTEL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARS-----EDSRPAAHFHLSSRRRHQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 KSRSSHSRSSSRSSSRSRSRSRSRSSSSSQSRSRSSSRERSRSRSSKSRSSSRSHR 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : : : | | : : | | : | : | 35 FARRISCNRCGREKTTEAKMMKAGGTEIGKTLAEKSRGLFSANDWQCKTCSNVNWARRSE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 FPAKATSTATAQRRTRQLIPLVLGFIGLGLVVA----ILALTIWQTTRVSHLDKELKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 6.2%; Score 135; DB 14; Length 330; 1 Similarity 21.2%; Pred. No. 0.014; 68; Conservative 48; Mismatches 108; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 132; DB 9; Length 391; 28.6%; Pred. No. 0.03; tive 31; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR APPLICATION NUMBER: 60/233,063
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,397
OR APPLICATION NUMBER: 60/232,399
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,399
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/241,808
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,808
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,826
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,786
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,786
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,721
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,721
OR FILING DATE: 2000-10-20
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OR FILING DATE: 2000-10-20
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; Patent No. US20020012968A1
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 68; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 44; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 391
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 13, 2004, 10:32:13; Search time 19 Seconds (without alignments) 2070.649 Million cell updates/sec Run on:

US-09-813-329-6 2162 1 MTABTLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	.2	hypothetical prote		chromodomain helic		histidine rich cal	homeotic protein c	probable transcrip	hypothetical prote			u	IFH1 protein - yea	probable peptide-a	hypothetical prote	zinc finger protei	MAK16 homolog PFB0	F8K7.2 protein - A	hypothetical prote	덫	uz	hypothetical prote	protein heat shock	polyprotein - Arab	_	nucleolin - Chines	hypothetical prote	ď
SUMMARIES		869625	A34373	S64951	A71623	T13944	T28635	A54660	803170	T18233	S19365	G71609	T21259	T03377	855352	T18861	A89959	T41390	G71621	A86349	T46237	T28156	T18402	T10215	Н96770	T31353	H84590	A27441	T16419	864603
	DB	7	7	7	~	~	7	~	٦	N	~	7	~	~	7	~	~	~	7	7	~	7	~	~	~	~	7	~	7	7
	Query Match Length		852	764	1192	1883	3097	669	2175	662	466	2500	775	692	1085	872	1274	463	432	709	1672	2910	3844	487	630	1390	406	713	1001	1379
٠	Query	7.7	7.1	6.7	6.4	6.4	6.4	6.3	6.3	6.2	6.2	6.2				9.9	υ 0		5.8		•	5.8			5.7	•	5.7	5.7	5.7	5.7
	Score	165.5	153.5	144.5	138.5	38	138.5	137	137	135	134	133		129	129	127	•	126	125	125	125	125	124.5	123.5	123.5	m	122.5	122.5	122.5	122.5
	Result No.		7	m	4	ស	φ	7	80	o	10	11	12	13	14	15	16	17	18	19		21	22	23	24	25	26	27		53

osteopontin precur	hypothetical prote	hypothetical prote	myoD protein inhib	gene suppressor-of	hypothetical prote	osteopontin precur	hypothetical prote	osteopontin precur	protein P120 - Myc	hypothetical prote	hypothetical prote	hypothetical prote	Ap-3 adaptor compl	protein kinase agg	hypothetical profe
809575	G86311	T30321	T03744	806028	B96695	A37818	B89921	GEPGO	T18352	B71609	H84463	T29776	T18295	S35423	G86155
н	~	N	7	~	~	Н	7	н	~	~	~	~	~	~	7
314	669	292	675	964	5138	294	6713	303	1078	665	770	1046	1105	1067	290
5.6	5.6	5.6	5.6	2.6	5.6	5.6	9.9	5.5	5.5	5.5	5.5	5.5	S. 5	5.5	5.4
Ŋ	21.5	121	120.5	120.5	120.5	120	120	119.5	119.5	119	119	118.5	118.5	118	117.5
121	Н														

ALIGNMENTS

RESULT S69625 hypoth C; Spec C; Date C; Acce	RESULT 1 S69625 Stypethetical protein YDR457w - yeast (Saccharomyces cerevisiae) C.Species: Saccharomyces cerevisiae C.Species: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 21-Mar-2001
Bubmir By Desc By Refe By Acce	Submitted to the EMBL Data Library, August 1995 A;Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787. A;Reference number: S69554
A, MOLO A, Res: A, Cros C, Gene	A;Molecule type: DNA A;Gross-references: EMBL:U33050; NID:g927726; PIDN:AAB64910.1; PID:g927738; MIPS:YDR457w C;Genetics:
A;Gen A;Cro A;Map	A.Gene: SGD:TOM1 A.¢ross-references: SGD:S0002865; MIPS:YDR457w A.;Map position: 4R
Que: Best Matc	Query Match Best Local Similarity 19.4%; Pred. No. 0.028; Matches 78; Conservative 66; Mismatches 142; Indels 117; Gaps 16;
ò	51 VAILALTIWQTTRVSHLDKELKSLKRVVDNLQQRLG1NYLDEFDFFQKEYE 101
q	1856 VAVEALNTISSTRNNFSEHFKIEDHDEVEDEVDESDKEIPDMFK 1900
δλ	102 NALIDYPKKVDGLTDBEDDDDGDGLDSIADDEDDDVSYSS 141
С	1901 NSALGMYDVEDIEEDDDDTSLIGDDAMAFVDSDNGFEVVFSDEDDDMGEED 1953
δλ	142 VDDVGADYTDMINKINNAHTGTTPTSETTAEGBGETDSASSASNDDNVFDDFTS 198
q	1954 ADDARSDSEE-NELSSEMQSSTADGTDVDYEVDDADGLIINIDQPSGDDEEMADYDANIS 2012
ò	199 YNAHKKKQERKSR8IADVRNEEQNIQGNHTELQEKSSNEATSKES 243
q	2013 HSSHSENEDDASMDVIEVYDDELS-SGYDVDLSDYDDESDWDSGLSSLSISDEDSESSE 2071
δ	244 PAPLHHRRRMHSRHRHLLVRKAR-SEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNER 302
д	2072 DEPINSTRMGDSRRWLIAEGVELTDDSQGESEED 2106
ò	303 NSYQGHEQIRDGVLTVINIGLXXVYAQICYNNSHDQNGFIVPQGDIPFLQCLNIVPIN 360
qq	2107 DRGVFRGIEHIFSNENEPLFRVHDEMRHRRNHHRSINRTHFHSAMSAPSLSLLNRGRRN 2164
ò	361 MPHKUHTCHTSGLIHLERIBERIHLKDI 387
qq	2165 QSNLINPLGPTGLEQVENDISDQVTVAGSGSRPRSHHLHFSEV 2207

a

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probable secreted protein PFB0115w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: N. V. Sizbou, E.; Suton, E.; Clayton, R.; Mite, O.; Koonin, E.V.;
Spertea, M.; Salzberg, S; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.,
Schence 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71620; MUID:99021743; PMID:9804551
A;Reference number: A71620
A;Accession: A71623
A;Accession: A71623
A;Accession: A71623
A;Scatus: DNA
A;Residues: 1-1192 cGAR>
A;Residues: 1-1192 cGAR>
A;Cross-references: GB:AE001373; GB:AE001362; NID:93845097; PIDN:AAC71813.1; PID:93845095
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: T13944
R;Stokes, D.G.; Tartof, K.D.; Perry, R.P.
Proc. Natl. Acad. Sci. U.S.A. 93, 7137-7142, 1996
A;Title: CHD1 is concentrated in interbands and puffed regions of Drosophila polytene chn A;Reference number: Z17823; MUID:96293489; PMID:8692958
QKEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDML 156
                                                                       646
                                                                                                                                               214
                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625 STDLDDQEEDGEEDKEDDKEKDKEDDKEKDKED------DKEKYK 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 EGEGETDSASSASND--DNVFDDFTSYNAHKKKOERKSRSIADVRNEEQNIQGNHTELQE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGYHG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723 KEDNKEKDKEDD-----KEKHDKHVRIKKKMKDDDYDES----LKTKNYYPHNMTFGQ 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 DMYIG--NDNERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQ---- 345
                                         SEEVGNSEDNEDDDTDEDSEDDDDDGGDDDSEDDDDDDD---GEGDENGDDGGG----
                                                                                                                                       157 NKLNNAHTGTTPTSETTAEGEGETDSASSASND-DNVFDDFTSYNA-HKKKQERKSRSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 GDTPFLQCLNTVP----TNMPHKVHTCHT-----SGLIHLERNERIHLKDIHND 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGIPKEQPYNNVPYILKKGLEPKTHN-HVKEDQPNIKQGVV---KGQEPHVDDMHNN 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              773 QQYFPYXNPLEQQNYQLHH------IIKQQQNYHPHHIIKQQQNHNPHHLLQEQEKHHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 DKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENAL----IDYPKKVDGLTDEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 ---- DDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79; Gaps
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                                                                                                                                                                                                                                                                                      DVRNEEQNIQGNHTELQEKSSNEATSK 241
                                                                                                                                                                                                                                                                                                                                       : ||:: : | | : : || ENFNEDETVADKDIEGGPESNKNSDSK 720
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A;Gene: PFB0115w
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hypothetical protein YLR114c - yeast (Saccharomyces cerevisiae)

hypothetical protein L2341

C; Adecesian: Saccharomyces cerevisiae

C; Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002

C; Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002

C; Accession: S6491; S63401

R; Verhasselt, P.; Voet, M.; Volckaert, G.

submitted to the Protein Sequence Database, May 1996

A; Reference number: S64943

A; Reference number: S64943

A; Residues: 1-764 <VER.

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A,Residues: 1-764 <VEW>
A,Cross-references: EMBL:X89514; NID:g1297019; PIDN:CAA61692.1; PID:e198747; PID:g129702
       A34373
histidine-rich calcium-binding protein precursor - rabbit
c;Species: Oryctolagus cuniculus (domestic rabbit)
c;Date: 08-Unn-1990 #sequence_revision 08-Jun-1990 #text_change 05-Nov-1999
C;Accession: A34373
R;Hofmann, S.1.; 0oldstein, J.1.; Orth, K.; Moomaw, C.R.; Slaughter, C.A.; Erown, M.S.
J. Biol. Chem. 264, 18083-18090, 1989
A;Title: Molecular cloning of a histidine-rich Ca(2+)-binding protein of sarcoplasmic r
A;Reference number: A34373; MUID:90036884; PMID:2808365
A;Accession: A34373
A;Accession: A34373
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-852 <4405>
A;Cross-references: GB:J05080; NID:g165099; PIDN:AAA31279.1; PID:g165100
C;Keywords: calcium binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 DEEDDDDGDGLDS-----IADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 DEDDDDEGDSTESDRHQAHRHRGHREEEDDDDD-----DDEG----DSTESDRHQAHRH 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 RGHREBEDEDDDBEGDSTESDRHQAHRHRGHREBEDEDDDEGDSTESDRHQAHRHRGHR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 TGTTPTSETTAEGEGETDSA------SSASNDDNVFDDFTSYNAHKKKQERKSR 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 SIADVRNEEQ------NIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRH 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 LLVRKARSEDSRPAAHFHLSSRRRHQGSMGYH----GDMYIGNDNERNSYQGH 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.1%; Score 153.5; DB 2; Length 852; Best Local Similarity 22.7%; Pred. No. 0.033; Matches 53; Conservative 31; Mismatches 88; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 764;
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A; Accession: 869401
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Thu Sep 16

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Gaps

16;

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Length 699;

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OMIM: 142705

243

-----RRRMHSRHRHLLVRK 264

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C;Species: Homo sapiens (man)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 05-Nov-1999
C;Accession: A54660
R;Hofmann, S.L.; Topham, M.; Haieh, C.L.; Francke, U.
Genomics 9, 656-669, 1991
A;Title: CDNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein, and lo A;Reference number: A54660; MUID:91244309; PMID:2037293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDDDDDDDDVSIEYRHQA-----HRHQGHGIEEDEDVSDGHHHRDPSHRHRSHEEDDN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 DVSYSSVDDVGADYEDYTDMLNKLNNAHTG-TTPTSETTAEGEGETDSA---SSASNDDN 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 VFDDFTSYNAHK--KKQERKSRSIADVRNE-----EQNIQGNHTELQEKSSNEATSKES
                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-699 <HOF>
A;Cross-references: GB:M60052; NID:g183918; PIDN:AAA88071.1; PID:g183919
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 EDEEVSAELGHQAPSHRQSHQDEETGHGQR--GSIKEMSHHPPGHTVVKD 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERNSY-QGHFQTRD
                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.3%; Score 137; DB 2; L
Best Local Similarity 20.7%; Pred. No. 0.29;
Matches 60; Conservative 38; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 DEFDEFQKEYENALIDYPKKVD---GLTDEEDDDDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 PAPLHH-----
                                                                                                                                                                                                                                                                      A;Gene: GDB:HRC
A;Cross-references: GDB:126369;
A;Map position: 19q13.3-19q13.3
C;Keywords: calcium binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 -----SYSSVDDVGADYEDYTDM------LNKLNNAHTGTTPTSETTAEGEGETDS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 ASSASNDDNVFDDFTSYN-----AHKKK------QERKSRSIADVRNEE 220
                                                                                                                                                                                                                                                                                           110 KVDGLTDEEDDDDGDGLDSIADDEDDVSYSSVDDVGADYEDYTDMLNK-LNNAHTGTT- 167
                                                                                                                                                                                                                                                                                                                               ------SSGSDSDSDAEGPSDQRNQSINNANTSSSL 128
                                                                                                                                                                                                                                                                                                                                                                         PTSETTAEGEGETDS----ASSASNDD-----NVFDDFTS-----YNAHKKKQE 207
                                                                                                                                                                                                                                                                                                                                                                                                   RKSRSIAD------VRNEEQNIQGNHTELQEKSSNEATS--KESPAPLHHRRRMHSRHR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 VDNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDDDGGGLDSIADDEDDDV 137
A;Status: preliminary; Lieuners A; Molecule type: mRNA A; Molecule type: mRD0. A; Cross-references: EMBL:L7907; NID:g1448982; PID:g1448983; PIDN:AAC37264.1 C; Genetics: A; Gene: CHD-1 A; Cross-references: FlyBase:FBgn0016132 A; Cross-references: FlyBase:FBgn0016132 C; Superfamily: chromodomain helicase CHD1; chromobox homology C; Keywords: DNA binding C; Corre 138.5; DB 2; Length 1883;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                   77; Indels
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23.7%; Pred. No. 1.4;
tive 33; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 HLLVRKARSEDSRPAAHFHLSSRRRHQGSMGY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRRVKPFSSEDSDDDASKRCATRRKGAAVSY 280
                                                                                                                                                                                                         Query Match 6.4%; Score 138.5; DE
Best Local Similarity 24.5%; Pred. No. 0.76;
Matches 52; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                   KTNGFTDDQEDSSSDG-
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Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                  129
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C,Accession: 503170
R;Blochlinger, K.; Bodmer, R.; Jack, J.; Jan, L.Y.; Jan, Y.N.
Nature 333, 629-635, 1988
A;Title: Primary structure and expression of a product from cut, a locus involved in spe
A;Reference number: S03170; MUID:88232956; PMID:2897632
A;Accession: S03170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: FlyBase:FBgn0004198
C,Superfamily: homeobox homology
C,Superfamily: homeobox; nucleus; transcription regulation
E,B86-958/Domain: cut repeat homology <CUs
F;1886-958/Domain: cut repeat homology <CUs
F;1617-1689/Domain: cut repeat homology <CUs>
F;1617-1689/Domain: cut repeat homology <CUS>
F;1617-1689/Domain: cut repeat homology <CUS>
F;1617-1689/Domain: homeobox homology <HOX>
                              C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-2175 <BLO>
A;Cross-references: EMBL:X07985; NID:g7767; PIDN:CAA30794.1; PID:g7768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
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homeotic protein cut - fruit fly (Drosophila melanogaster)
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Best Local Simi
Matches 64;
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RESULT 7 A54660 histidine rich calcium binding protein - human

NNINKKNTKKIKKKIHLKKKKVKPIPI 1810 QNIQGNHTELQEKSSNEATSKESPAPL 247

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RESULT 10 \$19365 bypothetical C;Species: { C;Species: { C;Accession R;Delgado, N R;	Query Matches Best Local Matches Qy 13 Qy 18 Qy 18 Qy 18 Qy 23 Qy 23	SULT 11 1609 Dothetic Spothetic Date: 13 Accessio Pertea, Title: 28 Accessio Referenc Referenc Residues Cross-re Experime Genetics Genetics Ouery Ma	DD 96 Qy 16
DD DD DD DD DD DD DD D	PESULT 9 T18233 probable transcription regulator protein - yeast (Candida albicans) C;Species: Candida albicans C;Saccession: T18233 R;Barrell, B.G.; Rajandream, M.A. R;Barrell, B.G.; Rajandream, M.A. R;Barrell, B.G.; Rajandream, M.A. A;Reference number: Z18831 A;Accession: T18233 A;Access	Query Match 6.2%; Score 135; DB 2; Length 662; Best Local Similarity 19.9%; Pred. No. 0.37; Death Collectivative 60; Mismatches 146; Indels 140; daps 19; Matches 86; Conservative 60; Mismatches 146; Indels 140; daps 19; An indels 140; daps 19; QY 67 LDKELKSL	Db 534 NSSHYMKKFDND 545

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type: DNA
11-2500 cGAR>
erences: GB:AE001408; GB:AE001362; NID:g3845238; PIDN:AAC71919.1; PID:g384524(
ital source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erences: EMBL:X59720; NID:g1907116; PIDN:CAA42379.1; PID:g5326; MIPS:YCL037C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 VSTISIEDL------DATRKKKN--RIPTPKSSTATKWVPIKASITVSGTKRSGSKNG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .86 ASNDDN------VFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNE 237 | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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al protein YCL037c - yeast (Saccharomyces cerevisiae)
Saccharomyces cerevisiae
-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
n: $19365
M.; Esteban, M.; Navas, L.
to the Protein Sequence Database, March 1992
e number: $19365
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1 Similarity 21.1%; Pred. No. 2.4;
69; Conservative 44; Mismatches 124; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78; Gaps
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1-466 <DEL>
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ZmHox1b causes pleiot

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Fireberlacker, B.; Klinge, B.; Werr, W.
Plant Cell 8, 349-362, 1996
A;Title: Ectopic expression of the maize homeobox genes ZmHoxla or ZmHoxlb ca A;Title: Ectopic author: Z14909; MUID:9631874; PMID:8721746
A;Accession: T03377
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Accession: T032 cUEB>
A;Cross-references: EMBL:X92428; NID:g1648930; PIDN:CAA63156.1; PID:g1648931
C;Genetics:
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C.Species: Gaenorhabditis elegans
C.Species: Gaenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Toot-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T21259
R.Wilkinson, J.
submitted to the EMBL Data Library, April 1996
A.Reference number: Z13397
A.Accession: T21259
A.Scatus: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-775 < WIL>
A.Residues: 1-775 < WIL-
A.Resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 SSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSY 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 --KKKLEAEAAAEAAKKKKQEEDDTGFDMFADNEELPQDSTTIDGHSGAVHDTLKDNWDD 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQGHFQTRDG-----VLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
T03377
Homeotic protein HOX1B - maize
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                     KKOERKSRSIADVRNEEQNIQG---NHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHL
                                                                                                                                                                                                             LVRKARSEDSRPAA--HFHLSSRRHQGSMGYH--GDMYIGNDNERNSYQGHFQTRDGVL
                                                                                                                                                                                                                                                                                                                                                     TVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75;
1021 SEEYTSEEYTSEGYTNEGYTNEQYINGQYINGQSIEDQSTNDQSIED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                       1191 SSENPNVDDLSGHI----QNNDNSFNSSSSNVP----LNVNPTNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.0%; Score 130.5; DB 2; Length Best Local Similarity 21.8%; Pred. No. 0.86; Matches 74; Conservative 49; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439 VEGYYRVRIGELLDTRYRVVGFTGAG---VFGNVCRCNDQTKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 VPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAVLR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ENSNILPLSIEGTNSAHLNFG--RSY 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 ERNERIHLKDIHNDRNAVLREGNNRSY 403
                                                                     204
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IPH1 protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein L8083.9; protein YER233c; RRP3 protein
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision
C;Accession: S55352; S5146; S47477
R;Cherel, I; Thuriaux, P.
R;Cherel, I; Thuriaux, P.
A;Title: The IFH1 gene product interacts with a fork head protein in Saccharomyces cerev
A;Reference number: S55352; MUID:95304839; PMID:7785326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 HKKKQERKSRSIADVR----NEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H---DEVSSPPLPDVKVGDMEKNTAQSNTTSSADDPMETEIDQSVVLPVSRRRQAERLDY 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLLVRKARSEDSRPAAHFHLSS-----RRRHQGSMG-----YHGDMYIGNDNER 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 KRLYDEAYGEASSDSSDEEEWSGKNTPIKSNEEGEVGSPAGKGSRVAHHNELTTONTKES 539
                                                                                                                                                                                                                                                                                                                                                                                                                      142 VDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNA 201
                                                                                                                                                                                                                                                                             91 DEFDEFOXEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDED----DD----VSYSS
                                                                                                                                                                                                                                                                                                                         317 NDFDPNMPEEHVA----SKEEGSSEEEEDDDG-GSDS--DDSDFLTCSDDLEPLIDKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 VDDLGLSSEDSED-----DDYDPAGPDSDKDVEKKSNSDESDFTSDSDDFCKEIKKSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cxoss-references: EMBL: 229488; NID: 9531491; PIDN: CAA82624.1; PID: 9531492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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A;Residues: 1-1085 <HAL>
A;Cross-references: EMBL:U19027; NID:g609363; PID:g609372; MIPS:YLR223c
A;Gene: Hox1b
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%; Score 129; DB 2; Length 1085; Best Local Similarity 19.9%; Pred. No. 1.6; Matches 73; Conservative 48; Mismatches 126; Indels 120;
                                                                                                                                     6.0%; Score 129; DB 2; Length 692;
22.9%; Pred. No. 0.93;
tive 37; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: The sequence of S. cerevisiae cosmid 8083
A;Reference number: S$1443
A;Accession: S$1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hallsworth, K. submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: SGD:S0004213; MIPS:YLR223c A;Map position: 12R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1085 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NSYQGHFQTRDGVLTVTNTGL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 LHSLHGSVDEXHGDLTSNGSNI 561
                                                                                                                                                                     Best Local Similarity 22.98
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259
                                                                                                                                            Query Match
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Db 331 HVSHREAQRLRRQHLRESRRDNRPRQGGNRECIHQDCPNRESLKPRKSLLVTKKKTKSMV 390 Qy 258 RHLLVRKARSEDSRPAAHFHLSSRRHQGSMG 289 Db 391 ERILDDEFDDEDDDEDDDSEVNKNDREDDDEDDVDERISDRDSSSSYKRHAITTKEEIG 450 Qy 290 YHGDMYIGNDNERNSYQGHFQTRDCVLTVTNTGLYYVYAQICYNNSHDQNGFI 342				
	RESULT 15 T18861 probable peptide-aspartate beta-dioxygenase (EC 1.14.11.16) - Caenorhabditis elegans C;5pciese: Caenorhabditis elegans C;5pciese: Caenorhabditis elegans C;Date: 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T18861, T23533 R;Swinburne, J. R;Swinburne, J. A;Reference number: Z19032	A,Accession: T18861 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Molecule type: DNA A,Residues: 1-872 <mil> A,Cross-references: EMBL:Z79596; NID:e1323798; PIDN:CAB01859.1; GSPDB:GN00028; CESP:K09A A,Experimental source: clone C02C6 R,Swinburne, J. Submitted to the EMBL Data Library, August 1996 A,Reference number: Z19753 A,Accession: T23533 A,Accession: T23533 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Rolecule type: DNA A,Residues: 1-872, WID.</mil>	A;Cross-references: EMBL:279601; PIDN:CAB01887.1; GSPDB:GN00028; CESP:K09A9.6 A;Experimental source: clone K09A9 C;Genetics: A;Gene: CESP:K09A9.6 A;Map position: X A;Introns: 18/1; 40/3; 74/1; 104/2; 139/1; 170/3; 385/3; 432/2; 464/3; 530/2; 609/3; 776 C;Keywords: oxidoreductase	Query Match 5.9%; Score 127; DB 2; Length 872; Best Local Similarity 22.9%; Pred. No. 1.6; 1.6; Matches 68; Conservative 48; Mismatches 109; Indels 72; Gaps 14; QY 88 NYLDEFDEFGKEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVD 143 Db 235 NQREEKKDKNKKYQPVKEEPDLDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 13, 2004, 10:23:02; Search time 12 Seconds (without alignments) 1774.724 Million cell updates/sec Run on:

US-09-813-329-6 2162 1 MTAETLKPFITPTSANDDGF.....DRNAVLREGNNRSYFGIFKV 409 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters:

141681 segs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	escription	P16230 ory	P23327 homo sapien	drosc		Q9beg5 bos taurus	Q92838 homo sapien			Q9xsy9 ovis aries	035986 rattus norv	P08199 mesocricetu	P40340 saccharomyc	P10451 homo sapien	Q9r020 mus musculu		drosc	mus	mus	Bus		Q8t5t1 giardia lam		-	P32583 saccharomyc	P53165 saccharomyc		043508 homo sapien		Q12019 Baccharomyc	P09405 mus musculu	P40480 saccharomyc	P53863 saccharomyc	
SUMMARIES	ID	SRCH RABIT	SRCH HUMAN	HMCU_DROME	SRO9_YEAST	EDA BOVIN	EDA_HUMAN	IFHI YEAST		OSTP_SHEEP	Z265_RAT	NUCL_MESAU	TBP7_YEAST	OSTP_HUMAN	Z265 MOUSE	Z265_HUMAN	SUWA_DROME	NRDC_MOUSE	OSTP_MOUSE	OSTP_PIG	A3B1_MOUSE	MDN1_GIALA	TUBE_DROVI	SGG_DROME	SR40 YEAST	YGG6_YEAST	HEX2_YEAST	TN12_HUMAN	MK21_YEAST	MDN1_YEAST	NUCL_MOUSE	HOS4 YEAST	YNW7 YEAST	NSR1_YEAST
	Length DB	852 1					391 1																					249	1025 1			m	90	14
a	Query Match L	7,1		•	6.2	•	•		5.9			•	•									5.5			5.4	5.4	5.4	5.4	5.4	•		5.3		
	Score	53	137	137	134	132	132	129	128	N	123.5	122.5	122.5	121.5	121.5	121	120.5	120.5	120	119.5	118.5	118.5	118	118	117.5	117	117	116	116	116		115.5	_	
	Result No.		7	Ю	41	ហ	9	7	8	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33

8193 saccharomyc 8996 saccharomyc	9214 plasmodium 4500 saccharomyc	1098 bos taurus 3306 saccharomyc	8709 xenopus lae 1096 bos taurus	3574 saccharomyc 3389 bos taurus	Q9c519 arabidopsis Q9nzw4 homo sapien
P36	P15	P31	P16	P45	09c
YBE6 YEAST	EBA1_PLAFC YMJ3_YEAST	OSTK_BOVIN BCK2_YEAST	VTA2_XENLA OSTP_BOVIN	GAT1_YEAST SG1 BOVIN	WRKG ARATH DSPP_HUMAN
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441 802	1435 899	277	1807	510 646	553 1253
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114.5	114.5	113.5	113.5	113	112.5
3.4	36	38	4 4 1	4243	4 4 5

ALIGNMENTS

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                                                                                                                                                                        ||:|||:|| :|
DEDDDDEGDSTESDRYQAHRHRGHREEDDDDD-----DDEG----DSTESDRYQAHRH 342
                                                                                                                                                          DEEDDDDGDGLDS-----IADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAH 163
                                                                                                                                                                                                                                                      212 SIADVRNEEQ-----NIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRH 259
                                                                                                                                                                                                                                                                             403 EEEDEDDDDEGDSTESDHHQAHRHRGHREEDEEDDDEGDSTESDRHQAHRHRGHGEBED 462
                                                                                                                                                                                                       164 TGTTPTSETTAEGEGETDSA-----SSASNDDNVFDDFTSYNAHKKKQERKSR
                                                                                                                                                                                                                             343 RGHREEEDEDDDDEGDSTESDRHOAHRHRGHREEEDEDDDDGGDSTESDRHQAHRHRGHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 9:656-669(1991).
-!- FUNCTION; May play a role in the regulation of calcium sequestration or release in the SR of skeletal and cardiac muscle.
-!- SUBCELLULAR LOCATION: Sarroplasmic reticulum lumen.
-!- SIMILARITY: STRONG, TO RABBIT HRC.
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                     260 LLVRKARSEDSRPAAHFHLSSRRRHQGSMGYH----GDMYIGNDNERNSYQGH 308
                                                                                                                                                                                                                                                                                                                     Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skeletal muscle,
MEDLINE=91244309; PubMed=2037293;
Hofmann S.L., Topham M., Hsieh C.-L., Francke U.,
"CDMA and genomic cloning of HRC, a human sarcoplasmic reticulum
protein, and localization of the gene to human chromosome 19 and
mouse chromosome 7.";
                                                                                                                                     61;
2-7.
2-8.
2-9.
2-10.
POLY-GLU.
POLY-GLU.
METAL-BINDING (POTENTIAL).
W; A43COCB3E494B930 CRC64;
                                                                                                             DB 1; Length 852;
                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sarcoplasmic reticulum histidine-rich calcium-binding protein
                                                                                                                                    Indels
                                                                                           7.1%; Score 153.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 142705; -.
GO; GO:0005509; F:calcium ion binding; TAS.
GO; GO:0006936; P:muscle contraction; TAS.
Calcium-binding; Signal; Repeat; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                          699 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANTS.
                                                                                    96117 MW;
                                                                                                                      22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M60052; AAA88071.1; -.
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
            423
451
470
585
733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
 368
396
424
452
471
721
780
852 AA;
                                                                                                                     Local Similarity
Les 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor.
HRC OR HCP.
                                                                                                                                                          116
                                                                                                                                                                                293
                                                                                  SEQUENCE
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                             463
REPEAT
REPEAT
                      REPEAT
REPEAT
                                                         DOMAIN
                                               DOMAIN
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P23327
                                                                                                                      Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                               193 EEEEEEEEEEEEEEEASTEYGHQAHRHRGHGSEEDEDVSDGHHHHGPSHRHQGHEEDDDDDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                              136 DVSYSSVDDVGADYEDYTDMLNKLNNAHTG-TTPTSETTAEGEGETDSA---SSASNDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 VFDDFTSYNAHK--KKQERKSRSIADVRNE-----EQNIQGNHTELQEKSSNEATSKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | :: | :: | :: | : : : | 306 DDDVSTEYGHQAHRHQDHRKEEVEAVSGEHHHHVPDHRHQGHRDEEEEDEDVSTERWHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --RRRMHSRHRHLLVRK
                                                                                                                                                                                                                                                                                                                                                                                         91 DEFDEFOKEYENALIDYPKKVD---GLIDEEDDDDGD------GLDSIADDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 DDDDDDDDDVSIEYRHOA-----HRHOGHGIEEDEDVSDGHHHRDPSHRHRSHEEDDN
                                                                                                                                                                                                                                                                                                                                                                76; Gaps
SARCOPLASMIC RETICULUM HISTIDINE-RICH CALCIUM-BINDING PROTEIN.
GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88232956; PubMed=2897632; Blochlinger K., Bodmer R., Jack J., Jan L.Y., Jan Y.N.; Blochlinger K., Bodmer R., Jack J., Jan L.Y., Jan Y.N.; Primary structure and expression of a product from cut, a locus involved in specifying sensory organ identity in Drosophila."; Nature 333:629-635(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 ARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERNSY-QGHFQTRD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota,
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha,
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                              1-4.
6 X APPROXIMATE TANDEM REPEATS.
2-2.
2-3.
                                                                                                                                                                                                                                                                                                                                    Length 699;
                                                                                                                                                                                                                                                                                                                                 ; Score 137; DB 1; Length 69;
; Pred. No. 0.16;
38; Mismatches 116; Indels
                                                                                                                                                                                                                                METAL-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                        Missing. -
/FTId=VAR_011622.
: 9922EEDF012C61DD CRC64;
                                                         TANDEM REPEATS,
                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                           FTId=VAR_005623.
                                          ACIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                   1-2.
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                                                                                                                                                                                                                                                                                                      80244 MW;
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                           204
261
365
270
318
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365
365
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177
237
294
673
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CT OR CG11387.
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                                                                                                                                                                                                                                                                                                    699 AA;
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STRAIN=Berkeley;
                           193
246
106
1106
238
2295
343
1106
1134
1155
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627
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us-09-813-329-6.rsp

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RAM MEDLINEZOUSGOOR, PURDREGALOTABLES,

RAMADER M. D., Celniker S. E., Holt R. A., Evans C. A., Gocayne J.D.,

RAMADER M. D., Celniker S. E., Holt R. A., Holtens R. A., Galle R. F.,

George R. A., Lewis S. E., Richards S., Abburner M., Henderson S. N.,

RAMADER M. D., Evanger S. E., Richards S., Abburner M., Henderson S. N.,

RAMADER M. D. Evanger S. E., Richards S., Abburner D. M., Henderson S. N.,

RAMADER M. D. Evanger S. E., Richards S. Champe M., Pfeiffer B.D.,

RAMADER M. Basu A., Basundal G. G., Gampe M., Pfeiffer B.D.,

RAMILW R. M., Basu A., Basundal G., Bayrakarcoglu L., Beasley E. M.,

Besson K. Y., Barne P. V., Berman B. P., Bandard D., Bolthakov S.,

RAM Burtis K. C., Buenm D. A., Buller H., Cadieu E., Center A., Chandra I.,

RAM Burtis K. C., Buenm D. A., Buller H., Cadieu E., Center A., Chandra I.,

Cherry J. M., Cavaley S., Dahlke C., Davenport L. B., Daviss P.,

RAM E Pablos B., Delcher A., Deng Z., Mays A.D., Dew I. Dietz S. M.,

RAM E Pobler C., Gabriellan A. E., Garge N. S., Dunkov B.C., Dunn P.,

RAM Harris M. L., Harvey D. A., Heiman T. J., Hernandez J. R., Houston K. J.,

RAM Harris M. L., Harvey D. A., Heiman T. J., Hernandez J. R., Houston K. J.,

RAM Harris M. L., Harvey D. A., Heiman T. J., Hernandez J. R., Houston K. J.,

RAM Harris M. L., Malbah F., Karpen G.H., Kz Z., Kennison J. A., Ketchum K. J.,

RAM Harris M. M. Halbah R. W. Honger D., Mostreif J., Moshrefi A.,

Roong F., Gorzell J. H., Gu Z., Gabby W. M., Mishina W. V., Mostrein D. R., Mostrein D. M., Malbahan W. V., Mostrein S., Mostrein D. M., Palazson D.,

Retnert K., Metel B., McInton H. V., Mostry C., Mucin M. H., Blang Y., Lin X.,

RAM Boon D. R., Mishina W. V., Mostry C., Wu D., Yang S., Yao Q. A.,

RAM Spiter B. Sprading A.C., Stapleton M., Stupski M.P., Smith T.,

Shene B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RAM Spiter B. Sprading A. C., Thrier R., Venter E., Wang S., Yao Q., A.,

RAM Shore B. S., Ramager E.W., Rubin G.W., Zhong S., Zho X., Zho X., Zhong S., Yao S., Yao S., Yao S., Yao S., Yao S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear (Probable).

TISSUE SPECIFICITY: Detected in many cells in the central nervous system, all external sensory organs, some peripheral neurons, and in the non-neural cells of the spiracles and the Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: Cell-specific pattern of expression. Broadly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed during embryonic development.

DOMAIN: Asn at position 47 of the homeobox may participate in regulating DNA-binding activity by promoting homo- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heterodimerization.
SIMILARITY: Belongs to the CUT homeobox family.
SIMILARITY: Contains 1 homeobox domain.
SIMILARITY: Contains 3 CUT domains.
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X07985; CAA30794.1;
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FlyBase; FBgn0004198; ct. GO; GO:0005634; C:nucleus; IDA.

AE003441; AAF46264.2;

PIR; S03170; S03170. TRANSFAC; T02004; -.

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: : | : | : | : | : | 312 TRTEPSATTQQQHQQDTEDLEENKDAGEASLNVSNNHNTTDSNNSCSRKNNNGGNESEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 HVASSAEDDDCANNYTNTSNNNYTSNTATSNT--NNNNNNNNSSSGNSEKRKKKNNNNNNG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 PAATVATGAAAAAAAATPIATGNVKSGSTTSNANHT---NSNNSHQDEE------ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 LQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 -----ELDDEEEDEEEDE-----DEDDEEENASMQSNADDMELDAQQE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 SVDDVGA------DYEDYTD----MLNKLNNAHTGTTPTSETTAEGEGETDS-- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNE--- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 PAKATSTATAQRRTRQLIPLVLGFIGLGLVVAILALTIWQTTRVSHLDKELKSLKRVVDN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 21.8%; Pred. No. 0.6;
Matches 64; Conservative 45; Mismatches 111; Indels 74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 QPAVLLAAKDKEIKALLDELQRLRAQEQTHLVQIQRLEE-----HLEVKRQH 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRH 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRO9 protein.
SRO9 OR YCL037C OR YCL37C.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 2175;
                                                                                                                                                      Nuclear protein; Repeat; Coiled coil.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
CUT 1.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                              ALA-RICH.
ASP/GLU-RICH (ACIDIC).
ASN-RICH.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
ALA-RICH.
HIS/GLN-RICH (OPA-REPEAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                              08BF80C4861BD0AB CRC64;
                                                                                                                                                                                                                           CUT 2.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                         ALA-RICH.
ASP/GLU-RICH (ACIDIC).
ALA/PRO-RICH.
                                                    pfam; PF02376; CUT; 3.
Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00011; HOMEOBOX 2; 1.
Transcription regulation; Homeobox; DNA-binding,
GO:0008587; P:wing margin morphogenesis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                    HOMEOBOX.
ALA/GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.3%; Score 137;
                                                                                                                                                                                                                                                        CUT 3.
                                                                                                                                                                                                                                                                                                                                                                                                                              2124 2136 ALA,
2175 AA; 233628 MW;
             InterPro; IPR007108; Cut homeo.
InterPro; IPR003350; Hmoeo CUT.
InterPro; IPR001356; Homeobox.
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                                                                                                                                                         protein;
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2014
2077
2136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                       Developmental
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                                                                                                                                                                                               DNA BIND
DOMAIN
                                                                                                                                                                                                                                                                     BIND
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63
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                                                            SEQUENCE
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TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 VSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSET------TAEGGGTDSASS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 VSTISIEDL------DATRKKKN--RTPTPKSSTATKWVPIKASITVSGTKRSGSKNG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 ATSKES-----PAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMG-- 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 ----YHGDMYIGNDNERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 ATSQENGQSTQQQQPPHHRNHHHSHH-----HNSNGPQRRKFHNSNNAGMPQNQGFP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 ASNDDN-----VFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNE
                                                   Kagami M., Toh-B.A., Matsui Y.;
"SRO9, a multicopy suppressor of the bud growth defect in the sackodaromyces cerevisiae RHO3-deficient calls, shows strong genetic interactions with tropomyces suggesting its role in organization of the actin cytoskeleton.";

Genetics 147:1003-1016(1997).

-I- FUNCTION: May overlap in function with tropomyosin and may be involved in organization of actin filaments. Acts as a multicopy
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDA BOVIN STANDARD; PRT; 391 AA. 09BEG5; Q9BEG5; C9BEG5; C9BEG5; C9BEG6; C8-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ectodysplasin A (Ectodysplasin I) (Ectodermal dysplasia protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              92; Indels
Delgado M., Esteban M., Navas L.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 AD8BB0895545117C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2%; Score 134; DB 1
21.4%; Pred. No. 0.15;
ive 32; Mismatches
                                                                                                                                                                                                                                                                                                                   GO; GO:0005844; C:polysome; IDA.
GO; GO:0003723; F:RNA binding; IDA.
GO; GO:0006412; P:protein biosynthesis; IPI.
InterPro; IPR006630; Lupus_La_dom.
Pfam; PFG5383; La; 1.
SMART; SM00715; LA; 1.
DOMAIN 200 203 POLY-GLN.
                                                                                                                                                suppressor of RHO3.
                                        MEDLINE=98043396; PubMed=9383048;
                                                                                                                                                                                                                                                                                                                                                                                                                466 AA; 51789 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 QGD----TPFLQCLNTV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 QQQFYPVQPVLMAINNI 297
                                                                                                                                                                                                                                                                          EMBL; X59720; CAA42379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 21.49
                                                                                                                                                                                                                                                                                    PIR; S19365; S19365.
GermOnline; 138873; -.
SGD; S0000542; SRO9.
                                                                                                                                                                                                                                                                                                                                                                                           203
258
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Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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EDA BOVIN
EDA BOVIN
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AC 28-FEI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21070494; PubMed=11167519; Droegemueller C., Distl O., Leeb T.; Droegemueller C., Proegemueller C., Droegemueller C., Droege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: N-glycosylated (By similarity).
-!- PTM: Processing by furin produces a secreted form (By similarity).
-!- DTM: Processing by furin produces a secreted form (By similarity).
-!- DISEASE: Defects in ED1 are the cause of anhidrotic ectodermal dysplasia. The disease is characterized by sparse hair (atrichosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
-!- SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ300468; CAC29151.1; -.

R EMBL; AJ300468; CAC29151.1; JOINED.
R EMBL; AJ300469; CAC29151.1; JOINED.
R EMBL; AJ300469; CAC29152.1; JOINED.
R EMBL; AJ300469; TNF_like.
R InterPro; IPR006052; TNF_like.
R Ffam; PF00131; COllagen; I.
R FFAM; SM00207; TNF; I.
R PROSITE; PS00251; TNF_l; FALSE NEG.
R PROSITE; PS00251; TNF_2; I.
M PROSITE; PS0049; TNF_2; I
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE (BY FURIN) (BY SIMILARITY)
CLEAVAGE (BY FURIN) (BY SIMILARITY)
COLLEGEN-LIKE.
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .)
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing, Named isoforms=2;
    Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sold=Q9BEG5-2; Sequence=VSP_006453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9BEG5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                        FROM N.A. (ISOFORMS A1 AND A2)
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                                                                   Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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160
229
313
372
308
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62
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DB 1; Length 391;

Score 132;

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8
                                                               264 KARSEDSRPAAHFHLSSRRRHQGS-MGYHGDMYIG--NDNER----NSYQGHFQTRDGVLT 317
                                                                                                           294
                                                                                                                                                318 VTNTGLYYVYAQ--ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                                                                                                                           295 VLVDGTYFIXSQVEVYXINFTDFASYEVVVDEKPFLQCTRSIETGKTN-YNTCYTAGVCL 353
                                                                                       Bayes M., Hartung A.J., Ezer S., Pispa J., Thesleff I., Srivastava A.K., Kere J., "The anhidrotic ectodermal dysplasia gene (EDA) undergoes alternative splicing and encodes ectodysplasin-A with deletion mutations in
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                            Gaps
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Van M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "X-linked anhidrotic (hypohidrotic) ectodermal dysplasia is caused mutation in a novel transmembrane protein.";
Nat. Genet. 13:409-416(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
MEDLINE-98349961; PubMed=9683615;
Monreal A.W., Zonana J., Ferguson B.W.;
"Identification of a new splice form of the EDA1 gene permits detection of nearly all X-linked hypohidrotic ectodermal dysplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM I), AND VARIANTS EDA HIS-61 AND LEU-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kere J., Srivastava A.K., Montonen O., Zonana J., Thomas N.S.T., Ferguson B.M., Munoz F., Morgan D., Clarke A., Baybayan P., Chen E.Y., Ezer S., Saarialho-Kere U., la Chapelle A., Schlessinger D.;
                                                                                                                                                                                                                                                                                                                                                                            EDA HUMAN STANDARD, PRT; 391 AA. 092613; Q9Y6L4; Q92638; C75910; Q9V6L0; Q9Y6L1; Q9Y6L2; Q9Y6L3; Q9Y6L4; Q1-NOV-1997 (Rel. 35, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ectodysplasin A (Ectodermal dysplasia protein) (EDA protein).
                          16;
                        63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDA
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"Expression of a novel transcript isoform of the umbilical cord.";
                                                                                                                                                                                                                                  LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM A1), AND VARIANTS
      0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
                     31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Hum. Genet. Suppl. 7:104-104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS A1; A2; B; C;
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    Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ations.";
J. Hum. Genet. 63:380-389(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Mol. Genet. 7:1661-1669(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Sweat gland;
MEDLINE=96331280; PubMed=8696334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98409495; PubMed=9736768;
28.6%;
                        44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagenous repeats.
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                    376
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                                                                                                                                                                                                                                                                                                                                    RESULT 6
EDA HUMAN
ID 092831
AC 092831
DT 10-0C
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OC BUKAR
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CHARACTERIZATION OF VARIANTS CYS-155; CYS-156 AND HIS-156, MUTAGENESIS OF ARG-153; LYS-158 AND ARG-159, AND CLEAVAGE SITE.
MEDLINE=21309995; PubMed=11416205;
Chen Y., Molloy S.S., Thomas L., Gambee J., Bacchinger H.P.,
Ferguson B.M., Zonana J., Thomas G., Morris N.P.;
"Mutations within a furin consensus sequence block proteolytic release of ectodysplasin-A and cause X-linked hypohidrotic ectodermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mutat. 17:349-349(2001).
-1- FUNCTION: Seems to be involved in epithelial-mesenchymal signaling during morphogenesis of ectodermal organs. Isoform Al binds only to the receptor EDAR, while isoform A2 binds exclusively to the receptor XEDAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Scarcity of mutations detected in families with X linked hypohidrotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS EDA CYS-156; HIS-156; CYS-255; ASP-255; GLY-274; TYR-332 AND
                                                                                                                                                                                                                                                                                                                        Elomaa O., Pulkkinen K., Hannelius U., Mikkola M., Saarialho-Kere U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ಡ
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"The mutation spectrum of the EDA gene in X-linked anhidrotic
                                                                                                                                                                                                      PROCESSING, MUTAGENESIS OF ARG-153, AND CHARACTERIZATION OF VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT EDA ARG-55.
MEDLINE-9939307; PubMed=10469321;
Martinez F., Millan J.M., Orellana C., Prieto F.;
Martinez F., Millan J.M., Orellana C., Prieto F.;
Martinez F., Millan J.M., Orellana C., Prieto F.;
Martinez Anhidrotic (Hypohidrotic) ectodermal dysplasia caused by novel mutation in EDA1 gene: 406T > G (Leu55Arg).";
J. Invest. Dermatol. 113:285-286(1999).
de Vos A.M., Gao W.-Q., Dixit V.M.; "Two-amino acid molecular gwitch in an epithelial morphogen that
                                                                                                                                                                                                                                                                                                                                                                                                            "Ectodysplasin is released by proteolytic shedding and binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Homotrimer.
-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=8;
Comment-Additional isoforms seem to exist;
Name=A1; Synonyms=II;
Isold=Q92838-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS EDA ARG-60, TYR-252, VAL-269; SER-302 AND MET-378. MEDINE-21272350; PubMed=11378824; Vincent M.C., Biancalana V., Ginisty D., Mandel J.L., Calvas F.Mutational spectrum of the ED1 gene in X-linked hypohidrotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferguson B.M., Thomas N.S.T., Munoz F., Morgan D., Clarke A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel missense mutation (402C-->T) in exon 1 in the EDA family with X-linked hypohidrotic ectodermal dysplasia."; Clin. Genet. 53:205-209(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hertz J.M., Noergaard Hansen K., Juncker I., Kjeldsen M., Gregersen N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 98:7218-7223(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ectodermal dysplasia: diagnostic implications."; J. Med. Genet. 35:112-115(1998).
                                                                           regulates binding to two distinct receptors."; Science 290:523-527(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Genet. 10:953-962(2001).
                                                                                                                                                                                                                                                                                  MEDLINE=21205766; PubMed=11309369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT EDA TYR-54.
MEDLINE=98292028; PubMed=9630076;
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MEDLINE=98168231; Pubmed=9507389;
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by Darwin.
     Name=B;
                                                                                  MIM; 300451
                                                          EMBL;
                                                                            EMBL;
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                                                                                 Genew;
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A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Bohnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Flocth M., Goffeau A., Hebling U., Hewnann K., Heusan K., Heusan K., Heusan K., Ansterfer D., Hilbert H., Hilger F., Kleine K., Koetter P., Anteler-Auer S., Nentwich U., Obermater B., Piravandi E., Pohl T.M., Anteler-Auer S., Nentwich U., Obermater B., Piravandi E., Pohl T.M., A Cortecalle D., Purnelle B., Rechmann E., Rieger M., Rinke M., Rose M., Charewood A.P., Urrestarazu L.A., Vandenbol M., Verlasselt P., A Unterwood A.P., Urrestarazu L.A., Vandenbol M., Verlasselt P., A Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D., Tr. nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

L. Nature 387:87-90(1997).
                                                                                                      264 KARSEDSRPAAHFHLSSRRRHQGS-MGYHGDMYIG--NDNER---NSYQGHFQTRDGVLT 317
                                                                                                                                                           240 KAGTRENOPAV-VHLOG----QGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELE 294
                                                                                                                                                                                                                318 VINTGLYYVYAQ--ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-mib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFH1 gene product interacts with a fork head protein in
        Score 132, DB 1; Length 391;
Pred. No. 0.17;
                                                             Indels
                                                             63;
                                                                                                                                                                                                                                                                                                                       376 LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                                                                                                                           |: ::| :| :| : ::|| ::| 354 LKARQKIAVKWVHADIS--INMSKHTTFFGAIRL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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                                                       31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FH1 protein (RRP3 protein),
FH1 OR RRP3 OR YLR223C OR L8083.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 28383 / FL100;
MEDLINE-95304839; PubMed-7785326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97313267; PubMed=9169871;
        6.1%;
28.6%;
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EMBL; U19027; AAB67412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae.";
Yeast 11:261-270(1995).
                                                       44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Thuriaux P.;
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GermOnline; 142285; -.
SGD; S0004213; IFH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: N-glycosylated.

PTM: N-glycosylated.

PTM: Processing by furin produces a secreted form.

DISBASE: Defects in EDI are the cause of ectodermal dysplasia, anhidrotic (EDA) [MIM: 305100], also known as X-linked hypohidrotic ectodermal dysplasia (XLHED). EDA is a disease characterized by sparse hair (atrichosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands. EDA is the most common form of over 150 clinically distinct ectodermal dysplasias. This disease was already described
                                                                                                                                                                                                                                                                                                                                Isold=Q92838-8; Sequence=VSP 006460, VSP 006461;
TISSUE SPECIFICITY: Not abundant; expressed in specific cell types
of ectodermal (but not mesodermal) origin of keratinocytes, hair
                                                                                                                                                                                                                                                                                                                                                                                                             follicles sweat glands. Also in adult heart, liver, muscle, pancreas, prostate, fetal liver, uterus, small intestine and umbilical chord.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SÍMILARITY: Belongs to the tumor necrosis factor family. SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                      IsoId=092838-5; Sequence=VSP_006458, VSP_006461;
             Isoid=092838-2; Sequence=VSP_006454, VSP_006455;
                                                                                                                    IsoId=Q92838-4; Sequence=VSP_006462, VSP_006463;
                                                                                                                                                                                                                           [soId=Q92838-6; Sequence=VSP_006456, VSP_006457;
                                                                                                                                                                                                                                                                                         VSP_006461;
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GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0007102; F:receptor binding; TAS.
GO; GO:0007105; P:sectoderm development; TAS.
GO; GO:0007105; P:sectoderm development; TAS.
InterPro; IPR008160; Collagen.
InterPro; IPR008163; TNF family.
InterPro; IPR00893; TNF family.
                                                                                                                                                                                                                                                                             IsoId=092838-7; Sequence=VSP_006459,
                                                                  IsoId=Q92838-3; Sequence=VSP_006464;
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AF060999; AAC36303.1; ---
AF060999; AAC36303.1; JOINED.
AF060994; AAC36303.1; JOINED.
AF060995; AAC36303.1; JOINED.
ALS80699; CAD18890.1; --
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1; APO61190; AAC77372.1; --
1; AFO61192; AAC77373.1; --
1; AFO61193; AAC77374.1; --
1; AFO61194; AAC77376.1; --
1; AFO61194; AAC77376.1; --
1; AFO61194; AAC77376.1; --
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EMBL;
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     12;
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                                                                                                                                                                                                                                                                                           262 ISFGNGNEGYNEDIGEEVLDLKOKENNGNEEDKLDSKVMLGNNDELRFPNISESDESE-- 319
                                                                                                                          KELKSLKRVVDNLQQRLGINYLDEFDEFQ-----KEYENALIDYPKKVDGLTDEEDDDDG 123
                                                                                                                                                 KKSKLIQRQIDNDDEG-----TESSDYQAVTDGEESENEEEESEEEEDDDEDDDDDD 147
                                                                                                                                                                                                                                                                         197 TSY-NAHKKKQERKSRSIADVRNEEQN------IQGNHTELQEKSSNEATSKESP 244
                                                                                                                                                                                                                                                                                                                          245 APLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGY-----HGDMYIGND 299
                                                                                                                                                                                                                                                                                                                                                   -----YDIDQDAYFDVINNEDSHGEIGTDLETGEDDLPILEE 356
                                                                                                                                                                                                                                                                                                                                                                           300 NERN------SYQG--HFQTRDGVLTVTNTGLYYVYAQ-ICYNNSHDQNGFIVFQ 345
                                                                                                                                                                                                                                                                                                                                                                                                   357 EEQNIVSELQNDDELSFDGSIHEEGSDPVEDAENKFLQNEYNQENGYDEEDDEEDEIMSD 416
                                                                                                                                                                                                                          161 NAHTGTTPTSETTAE--------GEGETDSASSASNDDNVFDDF
                                                                                                                                                                                                                                          DGSDSDSDSE-----TSSDDENIDFVKLTAQRKKRAMKALSAMNTNSNTLYSSRENSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97449184; PubMed=9285798; Ferguson B.M., Brockdorff N., Formstone E., Ngyuen T., Kronmiller J.E., Zonnama J.; Cloning of Tabby, the murine homolog of the human EDA gene: evidence for a membrane-associated protein with a short collagenous domain."; Hum. Mol. Genet. 6:1589-1594(1997).
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kere J., Schlessinger D.;
"The Tabby phenotype is caused by mutation in a mouse homologue of EDA gene that reveals novel mouse and human exons and encodes a protein (ectodysplasin-A) with collagenous domains.";
Proc. Natl. Acad. Sci. U.S.A. 94:13069-13074(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129/Sv;
MEDLINE=98058770; PubMed=9371801;
Srivaetava A.K., Pispa J., Hartung A.J., Du Y., Ezer S., Jenks T., Srivaetava A.K., Pispa J., Hartung A.J., Ko M.S.H., Thesleff I., Shimada T., Pekkanen M., Mikkola M.L., Ko M.S.H., Thesleff I., Kere J., Schlessinger D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                  48; Mismatches 126; Indels 120;
                                                                          DB 1; Length 1085;
GO; GO:0006348; P:chromatin silencing at telomere; IMP.
Oc); GO:0006364; P:rRNA processing; IGI.
Nuclear protein; Transcription regulation.
DOMAIN 122 163
DOMAIN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDA MOUSE STANDARD; PRT; 391 AA. 054593; 035705; Q9QW18; Q9QZ01; Q9QZ02; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ectodysplasin A (EDA protein homolog) (Tabby protein). EDI OR EDA OR TA. Mus musculus (Mouse).
                                                 1085 AA; 122491 MW; BEIC7DEF06213FE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3] SEQUENCE FROM N.A. (ISOFORMS TA-A2 AND TA-A3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS TAA; TAB AND TAC)
                                                                                     Pred. No. 0.85;
                                                                          6.0%; Score 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM TAD).
                                                                                      19.98;
                                                                                                73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           GDTPFLQ 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 FDMPFYE 423
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                 SEQUENCE
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GO:0045177; C:apical part of call; IDA.
GO:005789; C:andoplasmic reticulum membrane; IDA.
GO:000589; C:integral to plasma membrane; IDA.
GO:0007160; P:cell-matrix adhesion; IDA.
GO:0042346; P:positive regulation of NF-kappaB protein-nu. . .; IDA.
GO:0007411; P:salivary gland development; IDA.
                                                                                                               "Ectodysplasin, a protein required for epithelial morphogenesis, is a novel TNF homologue and promotes cell-matrix adhesion."; Mech. Dev. 88:133-146 (1999).

-!- FUNCTION: Involved in epithelial-mesenchymal signaling during morphogenesis of ectodermal organs. Isoform TRA binds only to the receptor EDAR, while isoform TA-A2 binds exclusively to the receptor XEDAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: N-glycosylated (By similarity).
-!- PTM: Processing by furin produces a secreted form (By similarity).
-!- PTM: Processing by furin produces a secreted form (By similarity).
-!- DISEASE: Defects in ED1 are the cause of the tabby phenotype in mice (the equivalent of anhidrotic ectodermal dysplasia in humans). The disease is characterized by sparse hair (atrichosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                          P., Kere J.,
                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Homotrimer (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008160; Collagen.
InterPro; IPR008052; TNF family.
InterPro; IPR008093; TNF_like.
Pfam; PF01301; Collagen; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS000251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF_2;
Differentiation; Developmental protein; Collagen; Transmembrane; Signal-anchor; Glycoprotein; Alternative splicing.
MEDLINE=20005791; PubMed=10534613;
Mikkola M.L., Pispa J., Pekkanen M., Paulin L., Nieminen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=O54693-3; Sequence=VSP_006469, VSP_006471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=054693-5; Sequence=VSP_006465, VSP_006468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=6;
Comment=Additional isoforms seem to exist;
Name=TAA; Synonyms=A1;
IsoId=OS4693-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=054693-4; Sequence=VSP_006466,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=054693-2; Sequence=VSP_006471;
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EMBL, AF016629, AAB95203.1; --
EMBL, AF016629, AAB95204.1; --
EMBL, AF016630, AAB95205.1; --
EMBL, AF016631, AAB95206.1; --
EMBL, AF04434, AAB8121.1; --
EMBL, AF004435, AAB8122.1; --
EMBL, X13438; CAA73849.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ243657; CAB52696.1; -. AJ243658; CAB52697.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=TA-A3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=TAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=TAD;
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154
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116 1
278 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z265 RAT
035986;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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ID Z265

AC 0359

DT 16-C

DT 28-E

DE Zinc

GN ZNF2

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                                                                                                                                                                                                                                                                                                                                                         264 KARSEDSRPAAHFHLSSRRRHQGS-MGYHGDMYIG--NDNER----NSYQGHFQTRDGVLT 317
                                                                                                                                                                                                                                                                                                                                                                     | : :::|| || || || 240 KTGTRENQPAV-VHLQG----QCSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELE 294
                                                                                                                                                                                                                                                                                                                                                                                              318 VINTGLYYVYAQ--ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                                                                                                                                                                                                                                                                                                                                                         295 VLVDGTYFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTN-YNTCYTAGVCL 353
                                                                                                     MALLINFFFPDEKAYSEEESRRVRRNKRSKSGEGADGPVKNK
KKGKKAGPPGPNGPPGPPGPPGPPGPPG1PG1PG1PGTTVM
                                                                                                                       GPPGPPGPPGGPPGLQGPSGAA -> VSHLGGAAALEAP
SPARLGGGLGLRAQGTLPLRAKFQGRSWEWAGVLGRGCPGQ
VVLGSCLGSSRPSPVPWSWRAQPARAAPGEVWAA (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Endometrium;
MEDLINE=99423513; PubMed=10491620;
Johnson G.A., Spencer T.E., Burghardt R.C., Bazer F.W.;
Johnson G.A., Cloning and expression of messenger ribonucleic acid in the uterus during the periimplantation period.";
Biol. Reprod. 61:884-891(1999).
                                                                                                                                                           /FTIG=VSP_006465.

PVENTKKKER -> KSTQVIFFP (in isoform TAB).
/FTIG=VSP 006466.
Missing (in isoform TAB).
Missing (in isoform TAB).
Missing (in isoform TAC).
/FTIG=VSP_006467.
                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                       /FTId=VSP 006470.
Missing (in isoform TA-A2 and isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryora, Metazos, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Caprinae, Ovis.
                                                             COLLAGEN-LIKE.
CLEAVAGE (BY FURIN) (BY SIMILARITY)
N-LINKED (GLCNAC. ) (POTENTIAL)
...TINGEN (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                      Score 128; DB 1; Length 391;
Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                       43; Conservative 31; Mismatches 64; Indels
                                                                                                                                                                                                                           (in isoform TA-A3).
 ECTODYSPLASIN A, MEMBRANE
ECTODYSPLASIN A, SECRETED
(BY SIMILARITY).
                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                  Frid-VSP 006469.
                                                                                                                                                                                                                                                                                         -> E (IN REF. 2).
ESECEDASBD60DEFF CRC64;
                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                            |: ::| :| :| :| :| 354 LKARQKIAVKMVHADIS--INMSKHTTFFGAIRL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                  LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                                                 FTId=VSP 006471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ostcopontin precursor (Bone sialoprotein 1).
SPPI OR OPN.
Ovis aries (Sheep).
                   SIMILARITY)
                              CYTOPLASMIC
                                                                                                                                                    isoform TAC
                                                                                                                                                                                                                                             Missing
                                                                                                                                                                                                                           Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                          126
41603 MW;
                                                                                                                                                                                                                                                                                                                       5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
 391
                           41
62
                                                       391
229
160
313
372
238
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                                                                                                                                                                                                                                              308
                                                                                                                                                                                                        391
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                                                                                                                                                                                                                                                                                         126 1
391 AA;
                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                            1
                                                      63
180
159
313
372
133
                                                                                                                                                                     169
                                                                                                                                                                                       178
                                                                                                                                                                                                       239
                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                               307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSTP SHEEP
Q9XSY9;
                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                 376
                                                                                 CARBOHYD
                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                      VARSPLIC
                                                                                                    VARSPLIC
                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                           CARBOHYL
                                                     DOMAIN
DOMAIN
SITE
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHEEP
                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 EFDEFQKEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDD----DVSYSSVDDVGA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | | : | | : | | : | | 10.2 DESDEADFPTIAVFTPPFPTESTNDGRGDSVAYGLKSKSKKFRRSNVESPDATEED 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTSH------IESSEMHDAPKKTSQLTDHSETNSDELPKELTPKAKES 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00017; OSTEO; 1.

PROSITE; PS00884; OSTEOPONTIN; 1.
Cytokine; Glycoprotein; Sialic acid; Biomineralization; Cell adhesion; Phosphorylation; Signal.

BY SIMILARITY.
                                                                                FUNCTION: Acts as a cytokine involved in enhancing production of interferon-gamma and interleukin-12 and reducing production of interleukin-10 and is essential in the pathway that leads to type SUBUNIT: Ligand for integrin alpha-V/beta-3.

SIBCELIULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 VLGFIGLGLVVAILALTIWQTTRVSHLDKELKS-----LKRVVDNLQQRLGINYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYEDYTDMLNKLNNAHTGTTP-TSETTAEGEGETDS------ASSASNDDNVFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VICECLLGIA---SALPVKPTSSGSSEEKQLNNKYPDAVATWLKPDPSQKQTFLEPQNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHS
FUNCTION: Binds tightly to hydroxyapatite. Appears to form an integral part of the mineralized matrix. Probably important to cell-matrix interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 278;
                                                                                                                                                                                                                                                                                      -1- PTM: Extensively phosphorylated on serine residues (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 123.5; DB 1; Length 23.3%; Pred. No. 0.38; ive 37; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSTEOPONTIN.
CELL ATTACHMENT SITE.
N-LINKED (GLCNAC. . .) (PK
                                                                                                                                                                                                                                                                                                                                                   -1- PTM: N- and O-glycosylated (By similarity).
-!- SIMILARITY: Belongs to the osteopontin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Zinc finger protein 265 (Zinc finger, splicing).
ZNF365 OR ZIS.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF152416; AAD38388.1; -. GO; GO:0005576; C:extracellular; ISS. GO; GO:0005125; F:cytckine activity; ISS. InterPro; IPR002038; Osteopontin. PF00865; Osteopontin; PRINTS; PR00216; OSTEOPONTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 RHRHLLVRKARSEDSRPAAHFH 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|: | |: || || || || KHSN---RIESQENSKLSQEFH 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31052 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 23.3 hes 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
278
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(Golden hamster)
                                                                                                                                                        FUNCTION.
MEDLINE=88312631; PubMed=3409881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1EJ7; 16-OCT-00.
PDB; 1FJC; 16-OCT-00.
INDB; 1FJC; 03-JAN-01.
INTERPRO; 1PR0005504; RNA_rec_mot.
Pfam; PP00076; rrm; 4.
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8
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2213
271
383
383
466
559
646
646
133
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A27441; A27441.
                                                 NCBI_TaxID=10036;
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81
81
89
103
118
126
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188
239
307
393
485
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548
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MOD_RES
MOD_RES
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REPEAT
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                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 KRVVD-----NLQQRLG------INYLD-----EFDEFQKEYENALIDYPKKVDG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTEL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 FPAKATSTATAQRRTRQLIPLVLGFIGLGLVVA----ILALTIWQTTRVSHLDKELKSL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 FARRISCURCGREKITEAKWAKAGGIEIGKILAEKSRGLFSANDWQCKTCSNVVWARRSE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRHQGSMG
                                                                                 Karginova E.A., Pentz E.S., Kazakova I.G., Norwood V.F., Carey R.M.,
                                                                                                    "Zis: a developmentally regulated gene expressed in juxtaglomerular
                                                                                                                         Am. J. Physiol. 273:F731-F738(1997).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: Expressed in kidney; more specifically renal juxtaglomerular (7G) cells.
-!- SIMILARITY: Contains 2 RANBP2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          90D6C7C3DE3A658F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 0.47;
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 08, Created)
(Rel. 08, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     RANBP2-TYPE 1.
RANBP2-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               ARG/SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 123.5;
                                                         STRAIN=Sprague-Dawley; TISSUE=Kidney;
MEDLINE=98042249; PubMed=9374836;
                                                                                                                                                                                                                                                                                                                                                                                          Zinc-finger; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01358; ZF RANBP2 1; 2. PROSITE; PS50199; ZF RANBP2 2; 2.
                                                                                                                                                                                                                                                                                                                    EMBL; AF013967; AAC02297.1; -.
InterEvo; IFR001876; Znf RanGDP.
Pfam; PF00641; zf-RanBp; 2.
SWART; SM00547; ZnF.RBZ; 2.
                                                                                                                                                                                                                                                                                            EMBL; AF013965; AAC02295.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                65 94 RJ
198 262 AJ
332 AA; 37837 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 20.4
nes 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Cr. 01-AUG-1988 (Rel. 08, Lat 01-OCT-2003 (Rel. 42, Lat Nucleolin (Protein C23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                             SEQUENCE FROM N.A.
                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCL MESAU
P08199;
                                                                                          Gomez R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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NUCL_MESAU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                        SEQUENCE OF 35-713 FROM N.A., AND SEQUENCE OF 1-34.

MEDLINE=87175501; PubMed=3470736;

Lapeyre B., Bourbon H., Amalric F.;

"Nucleolin, the major nucleolar protein of growing eukaryotic cells:
an unusual protein structure revealed by the nucleotide sequence.";

Proc. Natl. Acad. Sci. U.S.A. 84:1472-1476(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMAKT; SM00360; RRM; 4.
PROSITE; PS50102; RRM; 4.
PROSITE; PS00030; RRM RNP 1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
RNA-binding; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA TANDEM REPEATS OF X-T-P-X-K-K-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               decondensation by binding to histone H. ";

Eur. J. Biochem. 175:525-530 (1988).

-!-FUNCTION: Nucleolin is the major nucleolar protein of growing eukaryotic cells. It is found associated with intranucleolar chromatin and preribosomal particles. It induces chromatin decondensation by binding to histone H1. It is thought to play role in pre-rRNA transcription and ribosome assembly.

-!-SUBCELLULAR LOCATION: Nuclear; nucleolar.

-!-SIMILARITY: Contains 4 RNA recognition motif (RRM) domains.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomí;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erard M.S., Belenguer P., Caizergues-Ferrer M., Pantaloni A.,
Amalric F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A major nucleolar protein, nucleolin, induces chromatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRW) 1.
RNA-BINDING (RRW) 2.
RNA-BINDING (RRW) 3.
RNA-BINDING (RRW) 4.
ARG/GLY/PHE-RICH.
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METHYLATION (DI-).
METHYLATION (DI-).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
       the Swiss Institute of Bioinformatics and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1379 AA; 157406 MW; 31D1F6F87E62E04F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 -TRSSRHPETPPPVRRALRSRTRHSRTSNEEND--DENDNSRN 243
                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
POLY-GLU.
BROMODOMAIN (DIVERGENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 2.9; 40; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                        PIR; S64603; S64603.
GermOnline; 141582; -
SGD; S0003502; YTA7.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase.
InterPro; IPR003969; AAA_ATPase.
InterPro; IPR001360; AAA_ATPase.
InterPro; IPR001360; AAA_ATPase.
InterPro; IPR001360; AAA_ATPase.
InterPro; IPR003969; AAA_ATPase.
InterPro; IPR003969; AAA_ATPase.
InterPro; IPR003969; AAA, 1.
PROSITE; PS00674; AAA; 1.
PROSITE; PS00674; AAA; 1.
PROSITE; PS00674; AAA; 1.
ARP-Dinding; Bromodomain. 1; FALSE_NEG.
ATP-Dinding; Bromodomain. 2; 1.
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                                                   entities requires a license agreement (sor send an email to license@isb-sib.ch)
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POLY-ASN.
POLY-LYS.
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                                                                                       EMBL; Y07893; CAA69201.1; -. EMBL; Z73055; CAA97300.1; -. EMBL; X81072; CAA56963.1; -.
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11142
11153
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1016
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Best Local S:
Matches 53,
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NP_BIND
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                                                                                                                                                                        98 KEYENALIDYPKKVDGLTDEEDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLN 157
                                                                                                                                                                                                 133 KNGKNA-----KKEDSDEDEDDDDDDDDDDDBDBEBEED------EFEP---- 170
                                                                                                                                                                                                                                                                                       158 KLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNA-----HKKKQER-- 208
                                                                                                                                                                                                                                                 171 PVVKGKQGKVAAAAPASEDEDEEEBEEDEEEEDDSEEEEAMEITPAKGKKAPAKVV 230
                                                                                                                                                                                                                                                                                                                                               291 PEAKKOKVEGSESTTPFNL--------FIGNLNPNKSVAELKVAISEPFAKN 334
                                                                                                                                                                                                                                                                         209 --KSRSIADVRNEEQNIQGNHTELQEKSSNEATSKE-----SPAPLHHRRRMHSRHRH 259
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                                                                                                                                                     Gaps
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Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehnle S.,
Schwarzlose C., Vetter I., Feldmann H.;
"Identification of a set of yeast genes coding for a novel family
putative ATPases with high similarity to constituents of the 26S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C / FY1679,
Agostoni Carbone M.L., Lucchini G., Melchioretto P., Nardese V.,
Vanoni M., Panzeri L.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    63;
                                                                                                                           DB 1; Length 713;
                                                                                                                                                    Indels
 METHYLATION (DI-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                   40; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               procease complex.";
Yeast 10:1141-1155(1994).
-!- SIMILARITY: Belongs to the AAA ATPase family.
-!- SIMILARITY: Contains 1 bromodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-6CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
YTA7 OR YGR270W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1379 AA
                                                                                                                          5.7%; Score 122.5; 20.0%; Pred. No. 1.3
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STRAIN=S288C;
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| DLAVVDVRTGTNRKFGYVDFESAED 359
                                                                                                                                                                                                                                                                                                                                                                          DGVLTVTNTGLYYVYAQICYNNSHD 337
                                                                                                76997 MW;
                                                                                                                                                53; Conservative
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   665
669
673
679
                                                 681
687
691
                                                                                                                         Query Match
Best Local Similarity
                                                                                                  713 AA;
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Feldmann H.;
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TBP7_YEAST
ID TBP7_YEAST
AC P40340;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 KOERKSRS----IADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHL 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 GADYEDYTDMLN-KLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNAHKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 INYAEIEKVFDFLEDDQVMDKDETPVDVTSDEHHNNNQKG-----DDEDDDVDLVSPHEN
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Actauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                       Shiraga H., Min W., VanDusen W.J., Clayman M.D., Miner D.,
Terrell C.H., Sherbotie J.R., Foreman J.W., Przysiecki C.,
Neilson E.G., Hoyer J.R.,
"Inhibition of calcium oxalate crystal growth in vitro by uropontin:
another member of the aspartic acid-rich protein superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 89:426-430(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saitch Y., Kuratsu J., Takeshima H., Yamamoto S., Ushio Y.; "Expression of osteopontin in human glioma. Its correlation with the malignancy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and characterization of the human osteopontin gene and its
                                                                Kiefer M.C., Bauer D.M., Barr P.J.;
"The cDNA and derived amino acid sequence for human osteopontin.";
Nucleic Acids Res. 17:3306-3306(1989).
                                                                                                                                 MEDLINE=90353945; PubMed=1974876;
Young M.F., Kerr J.M., Termine J.D., Wewer U.M., Wang M.G.,
McBride O.W., Fisher L.W.;
"cDNA cloning, mRNA distribution and heterogeneity, chromosomal
location, and RPLP analysis of human osteopontin (OPN).";
Genomics 7:491-502(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hijiya N., Setoguchi M., Matsuura K., Higuchi Y., Akizuki S., Yamamoto S.;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Crosby A.H., Edwards S., Murray J.C., Dixon M.J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu W., Sarginson J., Gibbs R.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=95139605; Pubmed=7837791;
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MEDLINE=22388257; PubMed=12477932;
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                                                      MEDLINE=89263749; PubMed=2726470;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95031968; Pubmed=7945249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lochem. J. 303:255-262(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malignancy.";
Lab. Invest. 72:55-63(1995).
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                       SEQUENCE FROM N.A.
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              NCBI_TaxID=9606;
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326 3
326 AA;
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                                                                                                                                                                                                                                                                                                  64 EFINDFKQE-----TLPSKSNESHDHMDDMDDEDDDHVDSQDSIDSNDSDDVDDTDDS 117
                                                                                                                                                                                                                                                                                                                              139 YSSVDDVGADYED--YTDMLNKL--NNAHTGTTPTSETTAEGEGET------ 180
                                                                                                                                                                                                                                                                                                                                             -----DSASSASNDDNVFDDFTSY 199
                                                                                                                                                                                                                                                                                                                                                                                       NAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRH 259
                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | : | | : | | : | | ETHSHKQSRLYKRKA----FHSHEFHS-HED 283
                    SWART; SM00017; OSTEC; 1.

PROSTEE; PS00884; OSTECDPONTIN; 1.

Cytokine; Glycoprotein; Stalic acid; Biomineralization; Cell adhesion; Phosphorylation; Signal; Alternative splicing; Polymorphism.

SIGNAL 1 16 POTENTIAL.

CHAIN 17 314 OSTECDPONTIN.

SITE 159 161 CELL ATTACHMENT SITE.

CARBOHYD 79 79 N-LINNED (GLCNAC. ...) (POTENTIAL).

CARBOHYD 106 106 N-LINNED (GLCNAC. ...) (POTENTIAL).

WARSPLIC 31 57 Missing (in isoform C).

//PTIGHYSP 003777.

Wissing (in isoform B).
                                                                                                                                                                                                                                                                                     91 DEFDEFQKEYENALIDYPKK-----VDGLTDEEDDDGDGLDSIADDEDDDV----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams D.J., van der Weyden L., Kovacic A., Lovicu F.J., Copeland N.G., Gilbert D.J., Jenkins N.A., Ioannou P.A., Morris B.J.;
"Chromesome localization and characterization of the mouse and human cinc finger protein 265 gene.",
Cytogenet. Cell Genet. 88:68-73(2000).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Contains 2 RANBP2-type zinc fingers.
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                              DB 1; Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Zinc finger protein 265 (Zinc finger, splicing) (Fragment)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                 78; Indels
                                                                                                                                                     /FTIG=VSP_003778.

R -> H (In dbSNP:4660).

/FTIG=VAR 014717.

D -> H (IN REF. 7).

T -> A (IN REF. 7).

SHEF -> GNSL (IN REF. 2).
                                                                                                                                                                                                                                           5.6%; Score 121.5; DE 22.8%; Pred. No. 0.59;
                                                                                                                                                                                                                                                                 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLV--RKARSEDSRPAAHFHLSSRRRHQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Kidney;
MEDLINE=20237530; PubMed=10773668;
Pfam; PF00865; Osteopontin; 1. PRINTS; PR00216; OSTEOPONTIN. SMART; SM00017; OSTEO; 1.
                                                                                                                                                                                                                       35422 MW;
                                                                                                                                                                                                                                                    Local Similarity 22.8% es 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                      188
                                                                                                                                                                  301
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                                                                                                                                                                                                                       314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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CONFLICT
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SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 ETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTEL 230
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MEDLINE=99132651; PubMed=9931435;
Nakano M., Yoshiura K., Oikawa M., Miyoshi O., Yamada K., Kondo S.,
Miwa N., Soeda E., Jinno Y., Fujii T., Niikawa N.;
"Identification, characterization and mapping of the human ZIS (zincfinger, splicing) gene.";
Gene 225:59-65(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMG
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 66
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MEDINE-21154917; PubMed-11230166;
Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 PASILKEVEDKESEGEE---EDEDEDLSKYKLD--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36739 MW; 94593499E481FE88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 ----EDEDEDDADLSKYN----LDASEEEDSNKKKSNRRSRS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                EMBL; AF133818; AAF04474.1; -.
MGD; MGI:1858211; Zfp265.
InterPro; IPR001876; Znf RanGDP.
Pfam; PF0641; Zf-RanBp; 2.
SMART; SM00547; ZnF RBZ; 2.
PROSITE; PS01358; ZF-RANBP2 1; 2.
PROSITE; PS01359; ZF-RANBP2 1; 2.
ZinG-finger; Nuclear protein; Repeat.
ZN FING 9 40 RANBP2-TYPE 1.
ZN_FING 65 94 RANBP2-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.6%; Score 121.5; DE 20.4%; Pred. No. 0.62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Mismatches
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Job time : 14 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 KRVVD-----NLQQRLG-----INYLD------EFDEFQKEYENALIDYPKKVDG 113
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Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaler B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.;
"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
Genome Res. 11:422-435(201).
-! SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.6%; Score 121; DB 1; Length 337; 20.2%; Pred. No. 0.69; ive 47; Mismatches 94; Indels
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337 AA; 38223 MW; A4D20F6B3AD95925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Min; 0.04371; C:nucleus; TAS. GG; GO:0003723; F:RNA binding; TAS. GO; GO:0003700; F:transcription factor activity; TAS. GO; GO:0003380; P:RNA splicing; TAS. InterPro; IPR01876; Znf_RanGDP.
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                                                                                                                                                                                                                  IsoId=O95218-2; Sequence=VSP 004493; SIMILARITY: Contains 2 RANBP2-type zinc fingers.
                                                                                                                                                    Event-Alternative splicing; Named isoforms=2;
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                                                                                                                                                                   Name=ZIS-1;
IsoId=095218-1; Sequence=Displayed;
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1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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      plasmodium

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      Q8id27
      Q8id27
      Plasmodium

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      Q8ID2
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ALIGNMENTS

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RESULT 1

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ID OCCT-2002 (TTEMBLEEL: 22, Created)

DT 01-OCT-2002 (TTEMBLEEL: 25, Last sequence update)

DT 01-OCT-2003 (TTEMBLEEL: AT NP SEQUENCE UPROSODILIS UPPLINGENCE NEW NA SEQUENCE NEW NA SE
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                                                             MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGFIGLGLVVAILALTIWQ
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Moreno E., Yan M., Basler K.;
"Evolution of TNF Signaling Mechanisms. JNK-Dependent Apoptosis
Triggered by Eiger, the Drosophila Homolog of the TNF Superfamily.";
Curr. Biol. 12:1263-1268 (2002).
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Drocogene 22:4866-02033.

ENDIS AF521176; AAM76710.1; -...

R EMBL; AV115551; AAM66763.1; -...

R FYBASe; FBGH0031483; eiger.

R GO; GO:0016220; C:membrane; IEA.

GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:000555; P:immune response; IEA.

R GO; GO:000555; P:immune response; IEA.

R InterPro; IPR008983; TNF_like.

R SMART; SM00207; TNF_1.

R PROSITE; PS00021; TNF_1.

R PROSITE; PS00049; TNF_2: 1.

SEQUENCE 415 AA; 46918 MM; E087A26DE222D2BF CRC64;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Sutuppila S., Maaty W.S., Chen P., Tomar R.S., Eby M.T., Chan
Chew S., Rathore N., Zachariah S., Sinha S.K., Abrams J.M.,
Chaudhary P.M.,
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Last annotation update)
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           Mismatches
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EIGER OR CG12919 OR DARTH.
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
A patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Chiker S.,
Chouse S., Man K., Yu C., Lewis S.E., Rubin G.M.,
Chiker S.,
Chouse S., Man K., Yu C., Lewis G.M.,
Celniker S.,
Chouse S., Wan K., Yu C., Lewis G.E., Rubin G.M.,
Chouse S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Chouse S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Chouse S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Chouse S., Chambrane J. E.A.
Chouse S., Chambrane J. E.A.
Co. Go. 100 1839, AAN71595.1.
Chouse S., Chambrane J. E.A.
Co. Go. 100 1840 S., Summune response; IEA.
Co. Go. 100 1840 S., Immune response; IEA.
Chouse S., Chambrane J. Inkellike.
Chouse S., Chouse S., Chambrane J. Inkellike.
Chouse S., Chambrane
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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     8306AECCE14397B8 CRC64;
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Last annotation update)
                                               100.0%; Score 2162; DB 5;
llarity 100.0%; Pred. No. 1.4e-136;
Conservative 0; Mismatches 0;
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Pred. No. 3.1e-136;
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  46331 MW;
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Best Local Similarity
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                                                                                                    Matches 409;
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01-MAR-2003
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DT O1-M
DT O1-OC
DE NH51G
OC BENAN
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REALINE=20196006; PubMed=10731132;
REDINE=20196006; PubMed=10731132;
REDINE=20196006; PubMed=10731132;
REDINE=20196006; PubMed=10731132;
REDINE=20196006; PubMed=10731132;
REALINE=20196006; PubMed=10731132;
REALINE=20196006; PubMed=10.131132;
REALINE=20196006; PubMed=10.131132;
REALINE R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
REALINE R.A., Baxer B.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., Baxer B.G., Helt G., Nelson C.R., Miklos G.L.G., Rallew R.M., Basu A., Baxerdale J., Bayraktaroglu L., Beasley E.M., Bellow R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Berson K.Y., Benos P.V., Bernan B.P., Brottier P., Brottier P., Borchay J.M., Cawley S., Buller H., Cadieu B., Center A., Chandra I., Rallos B., Delcher A., Deng C., Davenport L.B., Davies P., Anderson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Perriera S., Fleischmann W., Rosler C., Gabriellan A.E., Garrell J.H., Gu Z., Galbart W.M., Glasser K., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Alasiali M., Kalush F., Kraft C., Kravitz S., Kulp D., Lai Z., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                    Length 415;
                                                                   Indels
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                  Query Match 99.4%; Score 2149; DB 5; Best Local Similarity 98.6%; Pred. No. 1.1e-135; Matches 409; Conservative 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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EIGER OR CG12919.
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Amerwilov G., Milshina N.V., Mobarry C., Morris J., Moshers in A.,
Mownt S.M., Moy M., Murphy B., Murphy L., Musny D.M., Nelson D.L.,
A palazzolo M., Pitturan G.S., Pan S., Pollard J., Puri V., Resee M.G.,
Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Turner R., Venter E., Wang X.,
Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Millams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Millams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
An illams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
M. Jobs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Cheng X.H., Zhong F.N., Zhong W., Zhong X.,
And Shong S.M., Woodage T.,
Sheng X.H., Arbang S.W., Wooley S.M., Wooley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 LNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRN
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EIGER OR CG12919.

Brosophila melanogaster (Fruit fly).

Brosophila melanogaster (Fruit fly).

Brosophila Mecazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 AA; 36862 MW; 6E5CCB69694F1A3A CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 AVLREGNNRSYFGIFKV 409
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Matches 310, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00251; TNF-
PROSITE; PS50049; TNF-
SEQUENCE 325 AA; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00207; TNF; 1
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69 KELKSLKRVVDNLQQRLGINYLDEFDEF----QKEYENALIDYPKKVDGLTDEEDDDDG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 KNLFVNMDSCNSWIVIKKSILINEYITRSQKND--LVDINDVLYDVVNMYHRIYNCYTRL 410
                  Mungall K., Bowman S., Arkin R., Baker S., Barron A., Brotter K.,

Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

Chillingworth T., Christodoulou Z., Clark E., Corton C.,

Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,

Relevell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

An Line A., Maddison M., Modlean J., Mooney P., Moule S., Murphy L.,

Aline A., Maddison M., Modlean J., Mooney P., Moule S., Murphy L.,

Aliane A., Sharp S., Smith R., Squares R., Squares R., Stevens K.,

Seeger K., Sharp S., Smith R., Squares S., Stevens K.,

Sulston J. B., Craig A., Newbold C., Barrell B.G.,

Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 D--DDYDDEDDDD--YEDDDD-----DDYDDDEDNYNNSYDNGYNTKHNKKKINPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 LSISNDHIEKEN--NLYIQNEQFINYDDVIFRKFK------FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 SSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRN-----EEQNIQGNHTELQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 YNSTIFETSNWNFCVKDEKRKKEKOKNSI-DKRNIIYSDDBSDNNYEHIFTHINSDLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 -KSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 GDMYIGNDNER-----YAQI--CYNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 HDQNGFIVFQGDTPFL-----QCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2226 AA; 267974 MW; 8690501ED4994768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.1%; Score 175.5; DB 5;
1.9%; Pred. No. 0.0062;
ve 57; Mismatches 150;
Churcher C.,
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 419:527-531(2002).
EMBL, AL034558; CAB38989.3, -.
InterPro. IPR007259; Spc97_Spc98.
Pfam; PF04130; Spc97_Spc98; 1.
Hypothetical protein.
Pain A., Berriman M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 21.9
1es 82; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRK-----ARSE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERNSYQGHFQTRDGVLTVTNTGLYYVYA 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLNKLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIA 60
         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
A Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George W., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Colliker S.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY119233; AAM51093.1;
R. FlyBase; FBGG1033483; eiger.
R. GO; GO:0005164; Fitumor necrosis factor receptor binding; IEA.
GO; GO:000555; P:immune response; IEA.
R. GO; GO:0005529; TNP_family.
R. InterPro; IPR000692; TNP_family.
R. SMART; SM00207; TNP_ilke.
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MEDLINE=99376085; PubMed=10448855;
MEDLINE=99376085; PubMed=10448855;
MEDLINE=99376085; PubMed=1048855;
Churcher C.M., Craig A., Davies R.M. Devlin K., Feltwell T.,
Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Horrscks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Rungall R., Murphy L., Ollver K., Quail M.A., Rajandream M.-A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodward J. R., Newbold C., Barrell B.G.,
"The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.9%; Score 1359; DB 5; Length 261; 97.7%; Pred. No. 3.8e-83; ive 0; Mismatches 0; Indels 6
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Eukaryota<u>;</u> Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 261 AA; 29780 MW; 13B6D5A04EC9122C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 24, Last annotation update)
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MEDLINE=22255708; PubMed=12368867;
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Best Local Similarity
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097225
AC 09722
AC 0972
AC 0972
DT 01-M
DT 01
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16;

85; Gaps

SEQUENCE FROM N.A.
MEDLINE=22255708; PubMed=12368867;
Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Alveolata; Apicomplexa; Haemosporida; Plasmodium Last sequence update) Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SGLIHLERNE 380
Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,

Cronin A., Davies R., Davies P., Dearden F., Doggett J.,

Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Harper D., Haueer H., Hornsby T., Holroyd S., Horrocks P.,

Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,

Oliver K., Ormond D., Price C., Quall M.A., Rabbinowitsch E.,

A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,

Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,

Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,

Sulston J. E., Craig A., Newbold C., Barrell B.G.

"Sequence of Plasmoddium falciparum chromosomes I, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 TELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGS 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 LDKELKSL----KRVVDNL----QQRLG--INYLDEFDEFQKEYENALIDYPKKVDGLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGETDSASSASNDDNVF----DDFTSYNAHKKKQ----ERKSRSIADVRNEEQNIQGNH
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Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCBL_TaxID=36329,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Mismatches 153; Indels
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Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Pred. No. 0.0099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 ------RIHLKDIHNDRNAVLREGNNRS 402
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EMBL; ALO31745; CAD49042.1; -.
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Best Local Similarity 21.2%;
Matches 83; Conservative 6:
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Devlin K., Baker S.,
Hall N., Bowman S., C
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8341 DDDDDDDDD-----DDYDEDYDEDYDEKLVENKKNERSNIIMSKENMKLNMQPK-N 8393
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Cronin A., Davies R., Davis P., Dearden F., Doggett J.,
Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
Harper D., Haucer H., Hornsby T., Holroyk S., Horrocks P.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Rnights A., Maddison M., Molean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares S., Stevens K.,
Sulston J.E., Craig A., Newbold C., Barrell B.G,
Squarec of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
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SEQUENCE 10061 AA; 1187600 MW; F13CE7E4FE86F3DD CRC64;
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InterPro; IPR006145; PseudoU_synth.
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Pfam; PF00917; MATH; I.
Pfam; PF00849; PseudoU synth_2; I.
PROSITE; PS00109; CYTOCHROME_C; I.
PROSITE; PS00109; EF_HAND; I.
PROSITE; PS00104; MATH; I.
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SEQUENCE
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1901 NSAL------GMYDVEDIEEDDDDTSLIGDDAMAFVDSDNGFEVVFSDEDDDMGEED 1953
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
Roberts D., Schramm S., Schracder M., Shogrer T., Shroff N.,
Winant A., Yelton M., Botstein D., Davis R.W.,
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 YNAHKKKQERKSRSIADVRNEEQNIQGNHTELQE-------KSSNEATSKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 PAPLHHRRRMHSRHRHLLVRKAR-SEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNER
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66; Mismatches 142; Indels 117;
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Utsugi T., Kikuchi Y.;
Utsugi T., Kikuchi Y.;
Utsugi T., Kikuchi Y.;
Utsugi T., Kikuchi Y.;
Usbali Ma-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U33050; ABA21482.1; -.
EMBL; D63905; BAA21482.1; -.
SGD; S0002865; TOMI.
SGD; S0002865; TOMI.
GO; GO:0007067; P:mitcosis; IMP.
GO; GO:0006937; P:muclear organization and biogenesis; IMP.
GO; GO:000693; P:nucleocytoplasmic transport; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3268 AA; 374180 MW; 8F71F3493D70A6C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dietrich F.S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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Pred. No. 0.046;
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InterPro; IPR008939, HECT_domain.
Efam; PR006129, HECT; L.
SWART; SW00119; HECT; 1.
PROSITE; PS50237; HECT; 1.
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Matches 78; Conservative 6
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MEDLINE=207;
MEDLINE=2255705; PubMed=12368864;
MEDLINE=2255705; PubMed=12368864;
MEDLINE=2255705; PubMed=12368864;
MATTALN=3D7;
MATTALN J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Sub. B., Peterson J., Angluoli S., Pertea M., Allen J., Selangut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B., Hoffman S.L., Newbold C., Davis R.W., "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TOBEDDOGOGLOSIADDEDDOVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                            2165 QSNLINPLGPTGLEQVENDISDQVTVAGSGSRPRSHHLHFSEV 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2026 AA; 244061 MW; A0261E55A6F47A14 CRC64;
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BMBL, AE014649; AAN36432.1; -.

GO; GO:000182; F:carboxypeptidase A activity; IEA.

GO; GO:0005489; F:carboxypeptidase A activity; IEA.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:000518; P:electron transport; IEA.

GO; GO:000518; P:electron transport; IEA.

InterPro; IPR000345; CytC, heme_BS.

INTERPRO; IPR000345; CytC, heme_BS.
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Last annotation update)
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361 MPHKVHTCHTSGLIHLE-
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
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01-MAR-2003
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NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 GDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSY 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701 KYLMKYKNIVISNINQ-----DHFNKKDYSNESEGEVNDFVKL-----DQSNINSRGS
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
PP10 0135.
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                     Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the human malaria parasite Plasmodium falciparum.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.4%; Score 160.5; DB 5; Length Best Local Similarity 19.6%; Pred. No. 0.066; Matches 70; Conservative 77; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE014850; AAN36480.1; -.
Hypothetical protein.
SEQUENCE 2309 AA; 276528 MW; 8A6F8DBB972C4922 CRC64;
                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                       2309 AA
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                                                                                                              Commercial (Trimble) 23, C 1.4MR-2003 (Trimble) 23, Li Hypothetical protein.
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                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 419:498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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01-MAR-2003
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                  RESULT 11
Q81517
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DT 01-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DQNGFIVFQGDTPFLQCLNTVPTNMPHKV-------HTCHTSGLIHLER 378
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                                                                                              I.T., James K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 DEEVDDDVESDDLKNKSKNKSKNKSKQDEKKKNPHDTEDDEDEDLNEEDEEENDED
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MEDLINE=22255705; PubMed=1236864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
                               Carlton J.M., Pail N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McRest J.C., Cummings L.M., Subramanian G.M., Mungall C., Fraser C.M., Barrell B.J., Hoffman S.L., Newbold C., Davis R.W., "Genome sequence of the human malaria parasite Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 159; DB 5; Length 491;
17.9%; Pred. No. 0.013;
tive 75; Mismatches 148; Indels
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NCBI_TaxID=36329;
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Last annotation update)
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MEDLINE=22255705; PubMed=12368864;
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EMBL; AE014831; AAN35333.1; -.
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 17.9%
Matches 70; Conservative
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Plasmodium falciparum
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Pfam; PF00092; vwa; 1.
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EMBL, AL644505, CAD54437.1; -..InterPro; IPR000894; TSP1.

InterPro; IPR002035; VWF.A.

Pfam; PF00090; tsp_1; 1.
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S. Perrea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B. Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A. McFaden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.1%; Score 154; DB 5; Length 2738; Best Local Similarity 21.0%; Pred. No. 0.22; Matches 82; Conservative 60; Mismatches 145; Indels 104;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
MAL6P1.261.
Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=36329;
                                                                                                                                                                                                                        "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00271; DnaJ; 1.
PROSITE; BS50076; DNAJ 2; 1.
Hypothetical protein.
SEQUENCE 2738 AA; 324824 MW; 9BDC29EE210E77B3 CRC64;
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Nature 419:498-511 (2002).
EMBL; AE014842; AAN36015.1; ..
InterPro; IPR001623; DnaJ N.
InterPro; IPR008941; TPR-Tike.
Fram; Pr00226; DnaJ; 1.
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DT 01-MA
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BDE HYPOT
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GN Plasm
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                                                                                                                                                                                                                                                                                          63 RVSHLD-KELKSLKRVVDNL-------QQRLGINY---LDEFDEFQKEYEN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NAHKKKQERKSRSIADVRNEEQN
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                                                                                                                                                                   Length 1371;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
                                                                                                                                                                Query Match 7.1%; Score 153.5; DB 5; Best Local Similarity 20.3%; Pred. No. 0.1; Matches 63; Conservative 53; Mismatches 93;
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SMART; SM00209; TSP1; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50092; TSP1; 1.
Hypothetical protein.
SEQUENCE 1371 AA; 160118 MW;
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nes 85; Conservative
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QEKSSNEATSKESP	MSKIMDINENFLFSNQNEEMNISTHNTSNNVTPPLLNNNINMNDDLKNIY 333	3	334 VNKNISTDFLKKNNFNVMINSPYYDSSNNSEQIQAKNKMEKNNKMYEASNPKMNNEKDKK 393	304 SYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQG 346	394 NVINIAGTKSSNTTSTNTFKFKKKYSSNFLKMFNKNIVKEYTSINTNNS 442	347 DIPFLQCLNTVPTNMPHKVHTCHTSCLIHLERNERIHLKDIHNDRN 392	:: SSVPLGRGESVDEVASDGIARDYS	
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AX642189 Homo sapi
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AE014831 Plasmodiu
AE014851 Saccharomyc
X89514 S. cereviala
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AC120096
AF158597
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-MODEL-frame+, pln. model -DEV=xlp
-MODEL-frame+, pln. model -DEV=xlp
-MODEL-frame+, pln. model -DEV=xlp
-Gen2 1/USFTO spool p/US09813329/runat_13092004_102753_21667/app_query.fasta_1.583
-DS-GenEmbl -QFWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=NO -THR MIN=0 - ALIGN=15 -MODE=LOCAL
-UNITS=bits -GTART=1 - THRESIZE=50 -MINEN=0 -MAXIEN=200000000
-USFR=US09813329 @CGN 1 1 7406 @runat_13092004_102753_21667 -NCFU=6 -ICPU=3
-NO MMAPP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBILCK=100 -LONCLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409
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(c) 1993 - 2004 Compugen Ltd.
                                                                                         - nucleic search, using frame_plus_p2n model
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Fgapop 6.0 , Fgapext
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                                                                                                                                                GluAsnAlaLeuIleAspTyrProLysValAspGlyLeuThrAspGluGluAspAsp
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          LeuGlnGlnArgLeuGlyIleAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyr
                                                                                         GACGATGGCGATGGTTCCATTGCGGACGACGACGACGACGTTAGCTATAGC
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S Igaki,T.
Direct Submission
Direct (02-NOV-2001) Tatsushi Igaki, Brain Science Institute,
RIKEN, Laboratory for Cell Recovery Mechanisms; 2-1 Hirosawa, Wako,
Saltama 351-0198, Japan (E-mail:igaki@brain.riken.go.jp,
Tel:81-48-467-6945, Fax:81-48-467-6946)
Location/Qualifiers
1. 1656
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Drosophila melanogaster mRNA for TNF superfamily ligand, Eiger, AB073865
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IGLGLVVAILALTIMQTTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYEN
ALIDYPKKVDGLTDEEDDDDDGGGLSTADDEDDDVSYSSYDDVGADYEDYTDMLNKLN
NAHTGTTPTSETTAREGGEGTDSASSASNDDNVFDDFTSYNAHKKKQBRKSRSIADVRN
BEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPANH
BLSSRRRHQGSMGYHGDMYIGNDDRRSYQGHPQTRGGVLTVTNTGLYYVYRQICYNN
SHDQNGFIVPGOSMGYHGDMYIGNDRRSYQGHPQTRGGVLTVTNTGLYYVYRQICYNN
AVLREGNNRSYFGIPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRN
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Aigaki,T. and Miura,M.
Eiger, a TNF superfamily ligand that triggers the Drosophila JNK
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                                                                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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2 (bases 1 to 2101)
Inohara,N. and Nunez,G.
Direct Submission
Submitted (10-MAY-1999) Department of Pathology, Comprehensive
Cancer Center, 1500 E. Medical Center Dr., Ann Arbor, MI 48109,
Location/Qualifiers
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            Drosophila melanogaster tumor necrosis factor family member DT1 (dt1) mRNA, complete cds.
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Drosophila melanogaster
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Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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Inohara,N. and Nunez,G.
DT1, a Drosophila tumor necrosis factor family
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                                                                                                                                                  GITTTGGGGTTCATCGGTCTTGGGGGCTGGTTGCCATTCTCGCACTAACGATCTGGCAG
                                                                                                                                                                                                    ThrThrArgValSerHisLeuAspLysGluLeuLysSerLeuLysArgValValAspAsn
                                                                                                                                                                                                                                                                                                                               CICCAGCAGCGITIGGGCATAAACTATCIGGACGAGTICGACGAGTICCAAAAGGAGTAC
                                                                                                                                                                                                                                LeuGlnGlnArgLeuGlyIleAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyr
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In Submitted (15-NOV-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley, CA 94720, USA Sequence submitted by:

Berkeley, CA 94720, USA Sequence Submitted by:

Lawrence Berkeley National Laboratory

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory

Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence 2000). The sequence has been subjected to integrity checks for sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accuracity principle particular cDNA clones that may have not been detected in our initial analyses such as internal priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAS, and reverse transcription of unspliced precursor RNAS, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to Location/Qualifiers

Location/Qualifiers

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                                                              Eukaryotta, Metazoda, Arthropoda, Hexapoda, Insecta, Pterygota;
Bukaryotta, Metazoda, Arthropoda, Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2165)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Patk, S.,
and Celniker, S., Pobuanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
Direct Submission
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/mol_type="mRNA"
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Matches:
Conservative:
Mismatches:
Indels:
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Drosophila melanogaster (fruit fly)
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                                                 Drosophila melanogaster
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FEATURES

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MetThralaGluThrLeuLysProPhelleThrProThrSerAlaAsnAspAspGlyPhe

. No.:

Met ProHisLysValHisThrCysHisThrSerGlyLeuIleHisLeuGluArgAsnGlu

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Percent Similarity:
Best Local Similarity:
 Alignment Scores:
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BEQNIQGNHTELQERKSNEATSKESPAPLHHRRPMHSRHRHLLVRKGBELLSARSEDS
                                                                                                                                  1248 bp mRNA linear INV 01-AUG-2003 DARTH (darth) mRNA, complete cds.
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QICYNNSHDQNGFIVFQGDTPPLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKD
IHNDRNAVLREGNNRSYFGIFKV"
 400
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Submitted (28-MAY-2002) Internal Medicine, UT Southwestern Medical
Center, 5223 Harry Hines Blvd., Dallas, TX 75390, USA
Location/Qualifiers
                                                                                                                                                                                              Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Bukaryota; Metazoza; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila,
I (bases 1 to 1248)
I (bases 1 to 1248)
Chew, S., Maaty, W.S., Chen, P., Tomar, R.S., Eby, M.T., Chapo, J.,
Chew, S., Rathore, N., Zachariah, S., Sinha, S.K., Abrams, J.M. and
Chaudhary, P.M.
Eiger and its receptor, Wengen, comprise a TNF-like system in
ArgileHisLeuLysAsplleHisAsnAspArgAsnAlaValLeuArgGluGlyAsnAsn
               /gene="darth"
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/note="Drosophila aspartate rich TNF homolog; tumor
necrosis factor ligand family member"
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178. .1245
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433. .438
433. .438
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Drosophila melanogaster
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Chaudhary, P.M.
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                                                                                                                             1 MetThrAlaGluThrLeuLysProPheIleThrProThrSerAlaAsnAspAspGlyPhe
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US-09-813-329-6 (1-409) x AF521176 (1-2159) Qy	ProblatysAlaThrSerThrAlaThrAlaGlnArgArgThrArgGlnLeulleProLeu 	uValvalalaileLeuAlaLeuThrileTrpGln 60	AspAsn GATAAT	Qy 81 LeuGlnGlnArgLeuGlylleAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyr 100	1 12 1	Qy 121 AspAspGlyAespGlyLeuAspSerIleAlaAspAspGluAspAspValSerTyrSer 140 Db 1001 GACGATGGCGATGGTCTCGATTCCATTGCGGACGACGACGACGACGACGACGATAGCTATAGC 1060	Qy 141 SerValAspAspValGlyAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsn 160	Oy 161 AsnalaHisThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThr 180	Oy 181 AspSerAlaSerSerAlaSerAsnAspAspAsnValPheAspAspPheThrSerTyrAsn 200	Oy 201 AlaHisLysLysGlnGludrgLysSerArgSerIleAlaAspValargAsnGluGlu 220	Oy 221 GlnAsnileGinGlyAsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThrSer 240	Qy 241 LysGluSerProAlaProLeuHisHisArgargArgArgHetHisSerArgHisArgHisLeu 260	Qy 261 LeuValArgLys	Oy 275 HisPheHisLeuSerSerArgArgArgArgHisGlnGlySerMetGlyTyrHisGlyAspMet 294	315 Va 315 Va 	Qy 335 SerHisAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGlnCysLeu 354
Db 901 TACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTTCAAACGCGGGATGGC 960 Qy 315 ValleuThkvalThkvalThkrGlyLeuTyrTyrValTyrAlaGln11eCysTyrAsnAsn 334	Oy 335 SerHishapGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGlnCysLeu 354	Qy 355 AsnThrValProThrAsnMetProHisLysValHisThrCysHisThrSerGlyLeulle 374	Oy 375 HisLeuGluarghsnGluargileHisLeuLysAspileHisAsnaspargasnalaVal 394	Qy 395 LeuArgGluGlyAsnArgSerTyrPheGly11ePheLysVal 409	RESULT 5 AF521176 LOCUS AF521176 LOCUS AF521176 AF521170 Drosophila melanogaster eiger mRNA, complete cds.	ACCESSION AF21116 VERNSION AF521176.1 GI:21717645 KEYWORDS Drogophila melanogagter (fruit flv)	ORGANISM Drosophila melanogaster (Interior 17) Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopteryopta; Diptera; Brachycera; Muscomorpha; Ebhydroidea; Drosophilidae: Drosophila		JOURNAL CURF. Biol. 12 (14), 1263-1268 (2002) PUBMED 12176339 REFERENCE 2 (bases 1 to 2159) AUTHORS Moreno. E Yan. M. and Basler K	TITLE Direct Submission JOURNAL Submitted (13-JUN-2002) Institut Molecular Biology, Uni Zurich, Winterthurerstrasses 190, Zurich, Z 8057, Switzerland FEATURES Location/Oualifiers	<pre>source 12159 //organism="Drosophila melanogaster" //mol_type="RRNA" /db_xref="taxon:7227"</pre>	CDS 641. 1888 // Codon start=1 // product=#eiger" / // Orotein id="AAM76710.1"	/db_xref="G1:21717646" /translation="MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGF IGLGLVVAILALTIWQTFRSHLDKELKSLKRVVNLQQREGNYLDREPEQKFPN A1:DYPKYUNG:TRDERDANDGROGE OF A ADDRESS AND AND A DATA AND AND A DATA AND A DATA AND A DATA AND AND A DATA AND A DATA AND AND AND AND AND AND AND AND AND AN	NATIGITETESETTARGEGETDGASGASUDDNYGAD 153 VDVAGATELI I IPPLINALN NATIGITETESETTARGEGETDGASGASUDDNYEDPTSYTAHKKQERKGRSI ADVRN EGNI QGHYTELOBKSSNEATSKESPAPLHHRRNMSRHRLLVRKGESLLSARSEDS RPAAHFHLSSRRRQGGAWGYHGDMYI GANNBRNSYGGHYUTVRYTKGLYYYYA OJCYNNSHDONGFI VROGTPPRI, OTANDENMSHKAHLCHTGGI TUT DDNGDE 111 VA		

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HRHLLVRKGESLLSARSEDSRPAAHFHLSSRRHQGSMCYHGDMYIGNDNERNSYQGH
FQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVH
TCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV"
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Best Local Similarity:
Query Match:
DB:
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Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
Berkeley, CA 94720
This clone was sequence date of a polyA tail and contiguity
Consequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription errors that result in single base changes. For further information about this sequence, including its location (http://fruitfly.berkeley.edu.) or send email to consequences.

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Stableton, W., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Stableton, W., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Glawpe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Pacel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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                                                                                                    394
                   AsnThrValProThrAsnMetProHisLysValHisThrCysHisThrSerGlyLeulle
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                                                                                                                       Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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full insert cDNA.
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170. .955
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Drosophila melanogaster SD18286 ful
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Drosophila melanogaster (fruit fly)
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1. .1221
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Db 32038 AATTIGCATTITAIGAIGGCAAACTCIGGCIAGGGIAICTCACAGICGGIAAGCCAIGCG 32097	66 66 Kō	Db 32098 CCTGTTTTTGAAAAGAATGCCTCAAAAAATGACCAGACGTAATATGTGGTTATTGTGT 32157	66 66 Kö	Db 32158 GGGACATACAAAAATATTTATAGAATTATGTGCTAAAATATAATTTCGACGCTGTTTCAT 32217	66 66 VO	Db 32218 CTGTTATTTGTTTCATTTTTTTTTTTGGCTGCCTTGGCCAAAGGCACATAGAAAATTGTG 32277	66 66 KD	Db 32278 ATAGATTATTTGAATTATAATGTCTCTTTCCGCAAGGAAACACTCATTTCAAATATGAGG 32337	66 66 VO	Db 32338 CGCCAGCCAGTTCACGTAATTTATGAGATACAAATCCCCCAAGTGACAAAAGGTAAAAGCC 32397	66	Db 32398 CCAATAATTCAACAAAAATACTAGGCTCTATCAGTAGATATAGTCGTTCAAGGCGAGCGA	66 66	32458 TCGCTTTTGGCTGTATGTGACGATTGATCGAATCTCAAATGGCCTAATGGCCAGAGA 32517	66 66	32518 IGGITITAAGAITITAAGAITTAITIATAITTTGAIGGCIGGGCAICIGIGGIGCCAAIT 32577	66 66	32578 CTCTTGAGAGTTTCCTTCGCTTTTAAATATATGTATGTACACAAGTATATGTATACG 32637	66 66	32638 AGTATCATGTTTTTGAGCGAGGCGCCATCAATTAGGATGATGACGAAACAGCCTGTGCTG 32697	66 66	32698 CGGGCGTGTCTCTAAAATGAACGTCCCAAATGGATGTGAGATATGTGCCAGGACTGTGC 32757	66 66	32758 CAGCTGCAGTCCACGTACTTGGCCAAGTCTTCTGACCCAAAATGCTGATGCCCATCCCTTC 32817	100TyrGludsnalaLeuIleAspTyrProLysLysValdspGlyLeuThrAspGl 117 	117 uGluAspAspAspGlyAspGlyLeuAspSerIleAlaAspAspGluAspAspVa 137	32878 GGAGGACGACGATGGCGATGGTCTGGATTCCATTGCGGACGACGACGACGACGACGT 32937	137 1SerTyrSerSerValAspAspValGlyAlaAspTyrGluAspTyrThrAspMetLeuAs	TAGCTATAGCTCTGTGGATGATGTTGGCGCAGACTACGAGGACTACACGGATATGTTAAA	157 nlysLeuksnAsnAlaHisThrGlyThrThrProThrSerGluThrThrAlaGluGlyGl 177 	177 uGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnValPheAspAspAspheTh	33058 GGGCGAGACGGACAGTGCATCCTCAGCCTCAAATGATGACAATGTCGTTCGATGACTTTAC 33117	197 rSerTyrAsnAlaHisLysLysLysGlnGlu
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ATCCACCTGGAACGAAACGAGGATCCATCTGAAGGACATTCACAACGATCGCA	ArgGluGlyAsnAsnArgSerTyrPheGly1lePheLysVal 409	GTTCTGCGGGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTG 952		1 melanogaster, *** SEQUENCING IN PROGRESS ***	GI:6223467	S PHASE2. a melanogaster (fruit flv)	melanogaster Metazoa: Arthi	Endopterygota; Diptera B: Drosophilidae; Dros	8 1 to 55359) and Venter I C	Direct Submission Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Dri	ified as CDM:10210834 by	ormation on this sequence you may	This is a 'working draft' sequence.	by the finished sequence as soon as it is available and the accession number will be preserved.	Location/Qualifiers 155359	/organism="Drosophila melanogaster" /mol type="qenomic DNA"	/db_xref="taxon:7227"			43.01% Conservative: 43.01% Mismatches:		x AC012854 (1-55359)	.euThr11eTrpGlnThrThrArqValSerHisLeuAspLysGluLeuL		LeulysArgValValAspAsnLeuGlnGlnArgLeuGlylleAsnTyrLeuAspG 	hedlnLysglu			CTCGGCGATGGGGCAGGGGCTGTAACATTTGCCCCGGGCAAATACAGATACCTCGA		TTTACAAAGTCGGAAATGATTGTTATTCCTTGAGGCTGGTACTTGAGTTTTTAATGAGG	TATATCGAACTITIGITATIGAGIATCTATTATGITTAGTITTCTTTTTGCCTAAAGGGT	
Db 845 ATCCACC	Oy 394 ValLeuA	Db 905 GTTCTGC	RESULT 7 AC012854		z	ω	NISM			TITLE Direct Su JOURNAL Submitted	Rockville, COMMENT This sequer	For	* NOTE: T	* *	FEATURES Source		ORIGIN	Alignment Scores:	Pred. No.: Score:	Percent Similarity: Best Local Similarity:	Query Match: DB:	US-09-813-329-6 (1-409)	Oy 54 LeuAlaLe	Db 31678 CTTATCT	Oy 74 LeuLysAı Db 31718 CTGAAGC		 Db 31798 GACGAGT	66 ХО	Db 31858 CTCGGCG	66	Db 31918 TTTACAAA	31978	66 KD

131444 CTAMPOCOMPOCOMPOCOMPOCOMPOCOMPOCOMPOCOMPOC		254 isSerArgHisheuLeuValArgLysAla
11164 CITANAGCARGICCOACTOACACAGGGGTTTCCCTATACATTCCAACAGGGTTTCCTATACAGGGTTC 1142	8 4 8 4 8 4 8 4 8 6 8 6 8 6 8 6 8 6 8 6	5 6 7 6 7 6 7
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Drosophila melanogaster

ENKaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Bohydroidea; Drosophila.

Ephydroidea; Drosophila.

Sa (lases 1 to 172904)

Callake, E. Wan, K. H., Baldwin, D., Kronmiller, B., Tyler, D., Wan, K. H.,

Holt, R. A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K. Y., Busam, D.A.,

Carlson, W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,

Ferriera, S., Frise, E. (Galle, R.F., Garg, N.S., George, R.A.,

Gonzalez, M. Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Kruse, D., Li, P., Matter, B., Moshrefi, A.,

Miltosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Phouanenavong, S., Pittman, G.S., Patel, S., Feiffer, B.,

Sayeri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Sayeri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Saveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,

Doyle, C.M., Farfan, D.E., Galle, R., Garge, R.A., Harris, N.L.,

Moshreff, A., Houston, K.A., Hummasti, S.R., Karra, K., Karra, K.,

Kim, E., Lee, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,

Rubin, G.M.

Rubin, G.M.
                                                                                                                                                 This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Meb site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                           172904 bp DNA linear INV 06-SEP-2001 Drosophila melanogaster, chromosome 2R, region 46C-46D, BAC clone AC007414
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Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Sep 6, 2001 this sequence version replaced gi:13324748.
                                                                                                                           375 isLeuGluArgAsnGluArgIleHisLeuLysAspIleHisAsnAspArgAsnAlaValL 395
                                                       enThrValProThrAsnMetProHisLysValHisThrCysHisThrSerGlyLeuIleH
                                                                                                                                                                                              Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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pbrosophia melanogaster BAC library, partial EcoRI
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Qy 266	RESULT 10 RESULT 10 AC099029, LOCUSS LOCUS LOCUS LOCUS AC099029 AC09029 163:16798961 PEFINITION Drosophila melanogaster, chromosome 2R, region 46D-47A, BAC clone ACCESSION AC09029 AC09029 AC09029 RESEARCH RESEARCH RESTRONCE BURATYCER, MELADOGA TATHORODGA; HEXADOGA; Insecta; Pterygota; Diptera;
137118 TCGCTTTTGGCTGTATGTGACGATTGATCGAATCTCATCAAATGGCCTAATGGCCAGAGA 137177 99	University Uni

Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibeqwam,C., Jalali,M., Kruse,D., Li.P., Mattei,B., Moshrefi,A	δο λο	66 66
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,	Db 165980	00 CCTGTTTTTGAAAAAAAATGCCTCAAAAAATGACCAGACGTAATATGTGGTTATTGTGT 165921
Photananavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,	6 YO	66 66
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Milliams, Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.	Db 165920	O GGGACATACAAAATATITATAGAATTATGTGCTAAAATATAATTTCGACGCTGTTTCAT 165861
TITLE Direct Submission JOURNAL Submitted (08-NOV-2001) Berkeley Drosophila Genome Project, MS	6 70	66 66
64-121, Lawrence Berkeley National Laboratory, One Cyclot: Berkeley, CA 94720, US	Db 165860	0 CTGTTATTTGTTTCATTTTTTTTTTTGCTGCTTGGCCAAAGGCACATAGAAAATTGTG 165801
COMMENT Sequence submitted by: Berkely Drosophila Genome Project	6 40	66 66
bawfeilce beikeley Nacional Laboratory, MS 64-121 Berkeley, CA 94720	Db 165800	00 ATAGATTATTTGAATTATAATGTCTCTTTCCGCAAGGAAACACTCATTTCAAATATGAGG 165741
Ints sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones.	Qy 9	66 66
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence	Db 165740	O CGCCAGCCAGITCACGIAAITTATGAGATACAAATCCCCAAGTGACAAAAGGTAAAAGCC 165681
	6 YO	66 66
FEATURES LOCATION/QUALITIEES Source 1. 189620	Db 165680	10 CCAATAATTCAACAAAAATACTAGGCTCTATCAGTAGATATAGTCGTTCAAGGCGAGGGA 165621
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DroBophila melanogaster BAC library, partial EcoR pBACe3.6)"	Qy 9	66 66
ORIGIN	Db 165500	0 CTCTTGAGAGTTTCCTTCGCTTTTAAATATATGTATGATGTACACAAGTATATGTATACG 165441
ment Scores: 2.52e-94	6 X0	
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09-813-329-6 (1-409) x AC099029 (1-189620)	Db 165380	CGGGCCTGTGTCTAAAAATGAACGTCCCAAATGGATGTGAGATATGTGCCAGGACTGTGC
Ov 54 [.e.,1,1]al.e.,ThrTleTrnGlnThrThrAroValSerHisle.,Benlong][.e.,1,08Ser 73	δδ	66 66
166400 CTTATCTTCCAGATCTGGCAGACAACGCGTGTATCGCATCTGGACAACGAGGCTTAAAGAAGAGAGTTCAAAGAAGAGAGTTAAAAGAAGAAGAAGAAGAAGAAGAAGA	Db 165320	CAGCTGCAGTCACGTACTTGGCCAAGTCTTCTGACCCCAAAATGCTGATGCCCATCCCTTC
	Qy 100	OTyrGluAsnAlaLeulleAspTyrProLysLysValAspGlyLeuThrAspGl
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66 66 XD	Oy 157	hivsLeuAsnAsnAlaHisThrGjyThrThrProThrSerGluThrThrAlaGluGjyGl 177
Db 166160 TTTACAAAGTCGGAAATGATTGTTATTCCTTGAGGCTGGTACTTGAGTTTTTAATGAGGG 166101		PANCICARACAN INCOMENCENCIA CANACANA INTERNATIVA INTONOMICANO INTONOMICANA INTONOM
66 66 AD	Db 165020	GGGGGACGGACGGACCTCCTCAGCCTCAAATGATGATGATGATGATGCTTTAC
Db 166100 TATATCGAACTTTTGTTATTGAGTATCTATTATGTTTTGTTTTTTTT		
66	164	
Db 166040 AATTTGCATTTTATGATGGCAAACTCTGGCTAGGGTATCTCACAGTCGGTAAGCCATGCG 165981	Qy 208	8

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233631 CTTATCTTGCAGATCTGGCAGACACGCGTGTATCGCATCTGGACAAGAGCAGGAGCTGAAGAGC 233690
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Direct Submission
Submitted (33-JAN-2003) University of California Berkeley, 539 Life
Submitted (33-JAN-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
On Jul 1, 2002 this sequence version replaced gi:10727672.
Location/Qualiflers
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Submitted (06-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 275390)
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                                    Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
5 (bases 1 to 275390)
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233991 TITACAMOTOGOAANTGTTUNTTCTUNTTCACTTCACCTTCACTTCTTTTACCTTCAAAGGGT 233930 QQ QQ QQ QQ QQ QQ QQ			177 uGlyGluThrAspSerAlaSerSerAlaSerAspAspAspAshValPheAspAspPheTh 197	235011	197 rSerTyrAsnAlaHisLysLysLysGlnGlu	235071	208	235130	216 lArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSerSerAs 236	235190	236 nGluhlaThrSerLysGlu 242		242 242		243		254 isSerArgHisArgHisLeuLeuValArgLysAla		265					235609 GGCGTCACCAAGGAAGTATGGGTAAGGAGATGCTTCCGCGTCAAGCGTGTACATACA	287		295 YIIIEGIYASnAppAsnGluArgAsnSerTyrGlnGlyHisPheGlnThrArgAspGlyv 315 235728 ACMARCANA	315 allenThrValThrAsmThrGlvfnentvormvythrValThrAshacidus Ca	235788 TCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACAACAACT 235847	335 erHisAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGlnCysLeuA 355	235848 CGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCATTCCTGCAGTGCTTGA 235907	355 snThrValProThrAsnMetProHisLysValHisThrCysHisThrSerGlyLeulleH 375	375 isLeuGluArgAsnGluArgIleHisLeuLysAspIleHisAsnAspArgAsnAlaValL 395		335
TTTACAAAGTCCGAAATGATTGTTATTCTTGAGGCTGGTACTTGAGTTTTTTAATGAGGG 213199 TATATACGAACTTTTGTTATTGTTATTGTTTTTTTTTTT	-	qa	۲۵ م	QQ	۵ ٥	qa	λ ₀	qu	ζō	<u>අ</u>	ờ	<u>옵</u>	ò	<u>අ</u>	<i>&</i>	Q	ò	a a	<i>&</i>	අු	δδ	qq	δλ	<u>අ</u>	λο ——	දු ර	<u>გ</u> წ	8 8	. q	<i>λ</i> δ	ପ୍ର	\trianslate{\delta}	ò :	3 è	χχ —
8 4 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5	g	233871 TTTACAAAGTCGGAAATGATTGTTATTCCTTGAGGCTGGTACTTGAGTTTTTAATGAGGG 23387	66 66	233931 TATATCGAACTTTTGTTATTGAGTATCTATTATGTTTTAGTTTTTCTTTTTGCCTAAAGGGT	66	233991 AATITGCAITITATGAIGGCAAACTCTGGCTAGGGIAICTCACAGICGGIAAGCCAIGCG 23405	66	234051 CCTGTTTTTGAAAAGAATGCCTCAAAAAATGACCAGACGTAATATGTGGTTATTGTGT		234111 GGGACATACAAAAATATTTATAGAAFTATGTGCTAAAATATAAATTTCGACGCTGTTTCAT		234171 CTGTTAFTTGTTTCAFTTTTTTTTTTGGCTGCTTGGCCAAAGGCACATAGAAAATTGTG 23423		234231 ATAGATTATTTGAATTATAAFGTCTCTTTCCGCAAGGAACACTCATTTCAAATATGAGG		234291 CGCCAGCCAGTTCACGTAATTTATGAGATACAAATCCCCCAAGTGACAAAAGGTAAAAGCC 23435	66	234351 CCAATAATTCAACAAAAATACTAGGCTCTATCAGTAGATATAGTCGTTCAAGGCGAGGG		234411 TCGCTTTTGGCTGTATGTGACGATTGATCGAATCTCATCAAATGGCCTAATGGCCAGAGA		234471 TGGTTTTAAGATTTTAAGATTTATTTATATTTTGATGGCTGGGCATCTGTGGTGCCAATT		234531 CTCTIGAGAGTTTCCTTCGCTTTTAAAIATGTATGTACGAACAAGTATATGTATACG	66	234591 AGTATCATGTTTTTGAGCGAGGGCGCCATCAATTAGGATGATGACGAAACAGCCTGTGCTG 2346		CGGGCGTGTGTCTAAAAATGAACGTCCCAAATGGATGTGAGATATGTGCCAGGACTGTGC 234	CAGC#GAB#Campament CAGC#	**************************************	GTTGCAGTACGAGAATGCCCTCATCGACTATCCAAAAAGGTGGATGGCCTCACGGATGA 23483	uGluAspAspAspAspGlyAspGlyLeuAspSerIleAlaAspAspGluAspAspAspVa 137	OGNOSTACIONOSTICIOS CONTINUES DE LA CONTINUE CARACCACICACIÓN (SA REGION SE LA CONTINUE DE LA CONTINUE DEL CONTINUE DE LA CONTINUE DEL CONTINUE DE LA CONTINUE DEL CONTINUE DE LA CONTINUE DEL CONTINUE DE LA CONTINUE DELA CONTINUE DEL CONTINUE DEL CONTINUE DEL CONTINUE DE LA CONTINUE DEL CON	TAGCTATAGCTCTGTGGGTGATGTTGGCGCGGAGTACGAGGACTACACCGATATGTTAAA 23495	157 nLysLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThrThrAlaGluGlyGl 177

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L. Nature 419 (6906), 527-531 (2002)
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                                                                                                                       INV 29-JAN-2003
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

I (bases 1 to 158548)

Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T.,

Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T.,

Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S.,

Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J.,

Moule, S., Munghl, K., Murph, L., Oliver, K., Quail, M.A.,

Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S.,

Sulston, J. E., Whitehead, S., Woodward, J.R., Newbold, C. and
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For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                Plasmodium falciparum MAL3P2, complete sequence.
AL03458 AL008982 AL008989 AL009007 AL009008 AL009014
AL010140 AL010150 AL010152 AL010156 AL010158 AL0102217
AL844502 297349 297350 298546
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3046. 3173,3308. 3388,3508. 3571,3699. 3737)
/gene="MAL3P2.1"
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/isolate="3D7"
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/chromosome="3"
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SGOTE 66.70, E-Value 4.88-16
Similar to Plasmodium vivax pv1h14090 pv1h14090w
SWALL:AAF99464 (EMBL:AY003872) (611 aa) fasta scores: E():
5.66-172, 71.94% id in 613 aa, and to Mus muscullus
5034406114riK protein 503406114riK SWALL:O9D308
(EMBL:AK017158) (368 aa) fasta scores: E(): 1.76-09,
24.87% id in 197 aa, and to Rattus norvegicus small rec
srec SWALL:Q9JKRS (EMBL:AF228917) (366 aa) fasta scores:
E(): 8.46-09, 27.95% id in 161 aa"
/codon start=1
/product="binding protein, putative"
/protein_id="CAB38988.3"
/db_xref="G12447021"
/db_xref="G12447021
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PPPKYKLI I HPTLLNVNEQNNSNI EI AREILYLGIY I RKI OKPI EI NKRSQSCNFTPD
I FCCCLSNI SAHILNHI NRI EENVRNI YNFTKI NMKHNSTNNYNNNNNNNHDNNNPI
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NKYENNDFWKYENIYGNDNIIKRSVQEEEEKKKWIEDNYNKESSLEFTYPYRKESGNRN
IFLIINSENINLGNSCYYNNDLIYIIHNNKRYEHMNLPKRTKKKKKKKKKRTKETKRK
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LLKNITTPLFDFIKNYIFYGKVKDTYKEPFIHENKHITPYYKQNHKPYFNNMYKYIPK
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LIDQNEYKNI NENI DI NMDTNQNNRNS PLFPKDVI YKR I YNENI NNDQYTNSDHI RNP
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                                                                                                                                                                                                                                              4 weak Pfam matches to entry PF00023 ank, Ank repeat; Pf. match to entry PF01529 zf-DHHC, DHHC zinc finger domain, score 66.70, E-value 4.8e-16
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join(1030. .2337,2429. .2502,2645. .2685,2826. .2941,
3046. .3173,3308. .3388,3508. .3571,3699. .3737)
/gene="MAL3P2.1"
                                                                                                                                                      /note="Revised: revised to 8 exon structure, revised:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 12790. .1323.9
| J9790. .1323.9
| // J960="PFC0166w" |
| 12790. .1329
| // J9700. .1329
| // J970. .1329
| // J970
                                                                                                                NENYHDOQVANNSENIESANAGASHANDUNQKQHYNEEYYKTKRERI IKKUAELLKUKGA
IKKKKI TYKKKGNYSKI.NEL RRNKNKTNNMMNNMMNNTNNNUDDINGSDELKNIK
NNFILKNI HINNNVENIMYETI YKCHILESYKMREPYNILENIT IT IKKTTILFRYINYK
Y IETKKLESWHILNHWYENIN IN INEECTRINIM CIHTRECHI HELKCYLYHIQUDVIKSE
YNNMNTKLKETLI FDDI IHIHNTYLNNI IKYSPIMDNI IT CILKLISI SHI FRHILI
KENEDKRUEQI ENI TIMHQWKSNYLNPNTTHINNHHHQYHNNKTNNRNNYHKKI IQE
LLLASYQNPTSFNNDI NESYYNDRFNDILLIFTYNNNI DEYAHNPLIKLDYNNYNNNYSKYNKH
KLSYQNPTSFNNDI NESYYNDRFNDILLDESYNNI DEYAHNPLIKLDYNNYNNYSKYNKHKKI IQE
SINNPI ESNSVQI KRKKKILLAMDRNYNNI DLINHTNI NDMNNI INLANNKGENYNLYREN
                  YLEKLYHYKKNNI LNKLKNFFDI SIRSSVLYHLKYKKDYNVAI SDI FSIMDNVNL I ID
LRKFQI SNEQQGLNKKGANNY EEVHDGDDDDDYYNNGNEYNNY EEGYNDDEEERNNY
                                                                                          LNKNDYDDEQEADDEBEDDDDDDDYDNDDDDEYKEYENDNGNDNYDEADSDHNNYNNT
                                                                                                                                                                                                                                                                                                                                                                                                                                    I TSE I KNHSPNEYRNNI I TNHT I NNNCNSNYHOINY SLHRFSNNNNNNNNNKKYOSEL.
HNLNDKSNFNKKDNYNI NDTNNNNYHYTNNNT SPKSSNEKNKI YNNHPI NYMRNDYNK
NI LNNNKOTI LSENPYLKEKNHI PFONKNHDTPSPLHI NNFNQDENNNI SPLNYSKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codom_start=1
/produc="thioredoxin-like redox-active protein, putative"
/protein_id="CA049085.1"
/db_xref="GI:23477023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tränslation="MACQVDNPPKTYPNDKTAEYEKYANYMNYLYYYQNNELKKIDSS
YFKDKYLGLFFGASWCKYCVTFIDSLNIFKKNFPNVEIIYIPFDRTYQEYGSFLKNTN
FYALPFDNYLYICKKYQIKNLPSFMLITPNNNILVKDAAQLIKTDEYINNLKSLIKNY
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biotin lipoyl, Biotin-requiring enzyme, score 46.20,
E-value 7.4e-10
Similar to Arabidopsis thaliana branched chain alpha-keto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similarity to lipoamide acyltransferases. eg
C.elegans lipoamide acyltransferase (WP:ZK669.4) BLAST
Score: 582, sum P(1) = 9.2e-57, 33$ identity in 430 aa
overlap; similarity to P. vivax PVH14105C, 59.908†
identity (61.611$ ungapped) in 434 aa overlap
Pfam match to entry PP00198 2-oxoacid dh, 2-oxo acid
dehydrogenases acyltransferase (catalytic domain), score
140.90, E-value 2.2e-38; Pfam match to entry PP00364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFNTSYNNNENIKNINLSNIDLDSIDNSRYSSKYNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GOA:Q81224"
/db_xref="SPTREMBL:Q81224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="synonym: PFC0170c"
complement (13855. .15201)
/gene="MAL3P2.3"
/EC_number="2.3.1.-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (13855. .15201)
/gene="MAL3P2.3"
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Alignment Scores: 0.433 Length: 158548 Score: 175.50 Matches: 82 Score: 37.17$ Conservative: 57 Best Local Similarity: 21.93$ Mismatches: 150 Query Match: 3.2$ Gaps: 16 US-09-813-329-6 (1-409) x PFMAL3P2 (1-158548)
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8

6174 6291 9689 5902 AATCAAGATTATCATGATAAAGACGATGATGATTATGATGATGAGATGATGATGAAGAT 5961 6231 6456 6510 143 ::: 5571 TATATTAATGATGATTTTTTGTTAATAAATAATAAGAAAGGAAATATTAGGTTCAA 6630 163 --GlnLysGluTyrGluAsnAla 103 ThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAspSerAla 183 302 CACAATGTGAATAATATAAAT---AATTATAACATGCGCGAACATTTAAAAAGGATAGAA 6747 291 321 ThrGlyLeuTyrTyrVal-----TyrAlaGlnIle-----CysTyrAsnAsnSer 335 HisThrSerGlyLeuIleHisLeuGluArgAsnGluArglleHisLeuLysAspileHis 388 144 AspValGlyAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHis -----GACACATTTGGTTCTGTTACTAGTATGAACGATGAAAAGGATTATATGAAATAT LeulleAspTyrProLysLysValAspGlyLeuThrAspGluGluAspAspAspAspGly 124 AspGlyLeuAspSerIleAlaAspAspGluAspAspAspValSerTyrSerSerValAsp SerSerAlaSerAsnAspAspAsnValPheAspAspPheThrSerTyrAsnAlaHisLys ---LysSerSerAsnGluAlaThrSerLysGluSerProAlaProLeuHisHisArgArg 5292 CTTAGTATTTCCAATGATCATATAGAAAAGAAAAT-----AATTTATATATATACAGAAT 252 ArgMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAspSerArg 3346 GAACAATTTATAAATTATGATGATGTTATTTTTTAGAAAATTTCAAA--------6631 AATGTTGCCTCACATATAAATAACACAACAAATAATAATATGAACAATATA 272 ProAlaAlaHisPheHisLeuSerSerArgArgArgHisGlnGlySerMetGlyTyrHis -----TTTCAT 292 GlyAspMetTyrIleGlyAsnAspAsnGluArg-----5457 CTTATTÄÄTGAATÄTATAACACGGTCACÄÄAAAAATGÄT-----TTÄGTAGATATAÄÄT ------GlnCysLeuAsnThrValProThrAsnMetProHisLysValHisThrCys 219 -----GluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGlu-----------AsnSerTyrGlnGlyHisPheGlnThrArgAspGlyValLeuThrValThrAsn 204 LysLysGlnGluArgLysSerArgSerIleAlaAspValArgAsn-----HisAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeu---389 AsnAspArgAsnAlaValLeuArgGluGlyAsnAsnArgSer 402 6391 -----TyrLeuAspGluPheAspGluPhe 369 352 6691 ò 셤 à Q

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Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Akkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrowa, C., Cherevach, I., Chillingworth, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Croin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Gahliam, R., Hamlin, N., Hanne, Z., Harper, D., Hauer, H., Hornsby, T., Holroyd, S., Larke, N., Kerbornou, A., Knighte, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Line, A., Maddison, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M., A., Rabbinowiesch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M., Sanders, M., Siamondes, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Stavens, K., Tayolor, K., Tivey, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.
            ::: |||| :::||||
73343 AAGAAAAGTAATTIGGTIAAAGAIAAGAAGAATAGTAGTAGTACCAGTACATGTAATAATIT 73402
                                                                                                                                                                                                                                                                                                                                     ||||||||::
73622 TTATTGAAGGCTAATACAATTGGTAATAATAATAATTCATATGAATAGTAATAATAATAAC 73681
                                                                                          73445 GCCTCTGATATGTATAATAAGGATACAAAT---ATGAGTTCATTAAATACCAGTGAAAAT 73501
                                                                                                                                                                                                                                                                        73561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313050 bp DNA linear INV 29-JAN-2003 Plasmodium falciparum strain 3D7, chromosome 5, segment 2/4. AL929352 AL644504 AL929352.1 GI:23504570
                                                                                                                                                 ------ValPheGlnGlyAspThrProPheLeuGlnCysLeuAsnThrValProThr 359
                                                                                                                                                                                                                                                                                                                -----SerGlyLeuIleHisLeuGluArgAsnGlu 380
                                                                                                                                                                                                                                                                                                                                                                                            Devlin,K., Baker,S., Davies,P., Mungal,K., Berriman,M., Pain,A., Devlin,K., Baker,S., Davies,P., Mungal,K., Berriman,M., Pain,A., Davlin,K., Bowman,S., Churcher,C., Quail,M. and Barrell,B.
Direct Submission
Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CBL0 189, UK
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                        :::||| ::: ||| 3502 ACTITACCTITATATATATATAGATTGTTCTGCTGTATTAGATATGAAATTATGG
                                                                   326 ValTyrAlaGlnIleCysTyrAsnAsnSerHisAspGlnAsnGlyPheIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                360 AsnMetPro---HisLysValHisThrCysHisThr-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Plasmodium falciparum 3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 ArgAsnAlaValLeuArgGluGlyAsnAsnArgSer 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/isolate="3D7"
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72989 GAAGATGACGACGATGACGAGTTATGACGATGATGATGACGAGGATTATGACGAAGAT 73048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73049 GAAGATGATGATGAGAATTACAATTTGAAGGATAAAAAAATTTGAAAGGTTTTGAA 73108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73109 AATAATAAGAGGATAAAAGGTAACAAGAAAGGTTCTGAGAAACCATTTGTTGTTATTAATAA 73168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 ValSerTyrSerSerValAspAspValGlyAlaAspTyrGluAspTyrThrAspMetLeu 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGlyLeuThrAsp 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 GluGluAspAspAspAspGlyAspGlyLeuAspSerIleAlaAspAspAspAspAsp 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 AsnLysLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThrThrAlaGluGly 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 ThrGluLeuGlnGluLysSerSerAsnGluAlaThrSerLysGluSerProAlaProLeu 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 HisHisArgArgMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSer 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 GluAspSerArgProAlaAlaHisPheHisLeuSerSerArgArgArgHisGlnGlySer 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 ArgLysSerArgSerIleAlaAspValArgAsnGluGluGlnAsnIleGlnGlyAsnHis 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 MetGlyTyrHisGlyAspMetTyrIleGlyAsnAspAsnGluArgAsnSerTyrGlnGly 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 HisPheGln-----ThrArgAspGlyValLeuThrValThrAsnThrGlyLeuTyrTyr 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::::||| ||| |||
72779 GAAGAAGAAGAAGAAAAATAGATGTTGAC------GATGTTGATGACGTTGACGAT
                                                                                                                                                                                                                                                                                                                                                                                                           --LysArgValValAspAsnLeu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GlnGlnArgLeuGly-----IleAsnTyrLeuAspGluPheAspGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnValPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 -----AspAspPheThrSerTyrAsnAlaHisLysLysLysLysGln------Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AAGAAGAAGAAGAAGCGTGTG
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83
61
153
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SKNKKONKGSDASFSSSDDTDDKLSSNKSELNYEENORKKONKKALLENHUDELDYIDI
KKNIYVQVKEITNMKDSDVDMFRKNNGNIIVRGKNCPRPVQYFYQCGLPSKILQILEK
KINIYVQVKEITNMKDSDVDMFRKNNGNIIVRGKNCPRPVQYFYQCGLPSKILQILEK
SIILTPTRELSIQVKTANKOSPVYLABATGSGKTLSYLEPVIRHVLHOBEPLRNNDGPI
SILITPTRELSIQVKTANLINRVSFVVLDEADRLLDGFESQIYNILENCKRÜKGVEILVGTPGR
IIDILTISNCKYTNLINRVSFVVLDEADRLLDGFESQIYNILENCKRÜKGYTANTSATF
PNYIQNMAKKLLYKPIEIVGEKKTNNNIYQFVEIIESKKVFRLLKLLGEWIKYGL
VILFUNKQIEDALLYLELYKTDYNLLVHGGQDQTDRQFTLEKFKKEBNKVLATSVM
ARGIDIKNIILVNINQCOMPIEDYIHRIGRAGNATGRANTGYRAYTLLPHSYTKAYDIYNL
LKNNIYYLNKTIDIPQDCPHIEDYIHRIGRAGNATGRANTGYRKKYTLDFPEKR
INNNNNNBEDDIKERKNLGLASSDDEGDSHSDSHSDSNSDSNSDSNSDSNSNS
HSDSNSNSHSDYSYKKKKHSHHSKYKKKHSHHRSKNKKKHSHHHSKKEKHISNDTHK
SDEKHRKYISSKKKKIKKEEKKKKNYHSKKMKYITYSNSSD"
                                                                                                                                                                                                                                                                                         /note="similar to Rattus norvegicus RNA helicase TR:Q62780 (EMBL:U25746) (1032 aa) fasta scores: E(): 2.4e-59, 38.387% id in 719 aa" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /procein_id="CAD51452.1"
| db_xref="G1:23504573" |
| db_xxef="GOA:091416" |
| db_xxef="GOA:091416" |
| db_xxef="SPTEMED:.091416" |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPSYAYKKKSSYHHVHREKYPDEKRKKYYEHICKKNKRRSYDYSSNYDESDFSSTSSY
YNERNKKYYKYEDKKKKEKEKEKEKERKRKKRYHHTDDDQDHLESYSSSRSSSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I KEKQKHKKLYSHEKERKRKKRYSNSANYSSYDEETKERDKKKKSYHHDFVLDDKKKN
YHNYESDEETNKDESNNNNNNNNNNNNNNKDSSSENLNKTHEQREKSININKISKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEI CEENKKEI QKVKENMSNVKVI TENNNLSR LERLÄLLFARK KKYNDTINERRYTTENNNLSR LERLÄLLFARK KKYNDTINERRYTKET LATKVNK INGAN FINDQDDBSDNSKEKEFDI KNENKI INVQNVDDNNHKODDTKKKI YE NHKKI KEDSINYNDIHVVEDEL RINKNEDBALDLFMKEI EGACEEBEKAVKKES TILDEI YYD MYKOKYE BF I NPKNHEE I KRYNKKKRIN QQSNI HEKQDSNVNTQEDLAKERKKNI YE NTTNNNY SDNNNNNDDDDDDDDDDDDDVPHKLFVEEKKYTEEDMKRATSSDLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKMNDTWELSLKAKKINELMKTYNFLSLQENHDKFLKNAQYEEFDKIAEKEALKVTËH
IKDEKEKKLI FINKTREDIKKKLIQNKIQSDTWINESIQRNMLLSALRTKNMKKYSPYLP
HTYITEDNNILLEFYINNYPQHYRLKISHKDYLAKIADMSGATCQIKGQYSNPSQPNK
QNFLLDTKQLHIELMPTYNQIQIRNELNSLLNNFNISCNIKAKRASTGWAPP"
COMPLEMENT (16598. .17442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVKESNI YPYTIHNSNNNMFEDKNSGI SKNMSKKNNTNEKKNTNQYTDI TKVEQEIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKSRKISMFKINLQNDFNYENKRFYNNMNRNVMNEKSLNKIMLIGRVGČEPDIKILNG
GDKVATFSLATNE FWRDRNTNELKSKTDWHRIVVYDQNIVDLIDKYLRKGRRVYVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHTRKWHTNDMNSQPKQITEIILSYNKGDLIFLDDKRNFNQRNNSNNINSENQQHINN
EHINNNNINNGNDFMPLNSNDKIIEDKEFTDRLDDNNEENNFQSNSETFDKQEGIYDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MGKRMLCIVFPLLIYFNYVLHRTYGYIIGDVKVHQLNNIINKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Weak similarity to Plasmodium falciparum Pfc0425W protein pfc0425W TR:077336 (EMBL:298547) (4550 aa) fasta scores: E(): 7.2e-23, 22.792% id in 3238 aa" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to Rickettsia prowazekii single-strand binding protein 8sb or rp836 SW:SSB_RICPR (092CC2) (15: aa) fasta scores: E(): 1.1e-16, 38.158% id in 152 aa Signal peptide predicted by Signal P. 2.0 HMM (Signal peptide probability 0.896, signal anchor probability 0.with cleavage site probability 0.471 between residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="single-strand binding protein, putative" /protein_id="CADS1453.1" /db xref="G1:33504554" /db_xref="G1:33504554" /db_xref="SPTREMBL:Q81415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="ATP-dependent RNA helicase, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (16588. .17442)
                                                                                                                                                                                                                                          'gene="PFE0430w"
                                                                                                                                                         /gene="PFE0430w"
11261. .15733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20022. .29426
/gene="PFE0440w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="PFE0435c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PFE0435c"
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/gene="PFE0440w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon start=1
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                                                                                                                           gene
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PTPFLEAPHYDNAGDNADDYDDDNANNSTYKRHKEDSIKWGYCHVHCGAGSKH
SLACKLHGDIYSWGYGGNGTLGLGANIKSYNKPOLIKGLRNKRILYVCAGTSHSGCID
NYNVYTWGNGKPYKLGHGNDDIDIYYPKLOLAHNKKVCMLSFGCFNSLALNYGGDV
SYWGTFNITUNYYNYISKLSKLPKQINYKCISLAHASTYVCGGTTLVODILSFGNYKNY
SYEKEINDNDSDDDILYKLINKEVEDRIYYNGDNKSYHTNKNIISSYNYKKTOBHFDI
HYIKENRGKMYIKDIYTHFYNLDTWTYWNKINKHIDNYTLNNNDNYYTYDNINGSHG
ILLNICYNKIIKINGSDDBIRSPHLKKFGYPAGYNKOBEGGUSENLKKKFGVP
ILLNICYNKIIKINGCTNYYLCVSGNYCHONGGGLGGTGVIDPYNKNLT
NVINIPAGYDHSACIINKLLDKGNYNVNNNNNNUNGSNGCOLGIGVIKDPYEPVHYNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGKVGLGVDYTQGCILLPRKINI INKIYKCSLGNSHSLFLTNYNELYVCGSNNNGRLG
LFEKSROWCKTVSVPTKVILHNNIYIKDLAGNTYS ILLSODEFIXTFGEFIKGSNGN
LREEKSROWCHYSVPTKYILHNNIYIKDLAGNTYS ILLSODEFIXTFGEFIKGSNGN
IKKPKLITYFLKENNKIIESIFSFHVYTFIQPNKLFGIGNNWNCQILCDNEKENNY
IKKPFKLITYFLKENNKIIESIFSFHNYTFIQPNNSEIFAMGYTNNTHLCIGIPNNIK
LKTPFTKIITYFGKLDDLDYNGSCSDMELMEYNTYNMGYTNNTHKINITILDTLVKKNI
NTTELFONNIYTYFGYYSEEIENFIYNIYIMNIINWCHLQNLLKKEEYNNMGYIKSF
RKDIIDLYSKHIEVLINLINIYEKQFNYLYLMNONTHLSPRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I FDONRIKLEOFIY I I QOOPVYLI I LCLI HNYKNYKOLMYGKMYSYNSNKNTTHIY
HNNINEQHIKNNYNI I NSNY I NHTYNY EQNDALKKYNSKD I ONKKYSFYKNSSNVLCS
FI FDLYADFRNERVRTIFTI FLIKLGIBEI KNSLANYKSIFNI DTSI FFTLI QMLFFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGNSCNQLGLGINNRFVNNPTVVCFFDSFIVASICCTNYATFVLVKKNVNDIGCSVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFFYNEHNFKNDIGLPSDDDIYDDYNISGDESLLNFEADNISSIONEDTNMDEDYYNN
IVNDHTNEDRQSDINETIDKHSNDNDYDDEKKKEKMNIYKNKEKLYSNIKENDNKHDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MYEQDDEDKDIHKYIFPFFPKISTGLDHYACVAYYKNKPSIFTW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGKGNNGLLGYKKKRELPNFLEHEEKKNIQKVKEQMLQKVNDPLNQMVLDAFGIKKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEKEKKKKKKKNDIKKEEKEENNINNEKKNNNNNNINSEKKKKNDINGHEAKYVQNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKDKEFLNFIKGKTQNESDKKRLFVNDISCYKSGVPYNIPNINMEDENMYRNNISQET
QNENLDNNDNYVEINFVCIFEELCKIFLNIKFPDMFKIIIKELFKYFIIYEKNLNDEI
NQTNKIYFYQNHHTIYIPFFKLILMAIINPILKNMENIAHKFSYPNIFPHILNIRNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDFLEILYLNKYESLNIYNLNIISIKYIFEHTFISLTNVINNICNTHHHIYVDAYTNL
FHYHLNRNSYYVQLKLFQVCHIFNLFFRFQNYLMLSFNDPALDIVNFFYTYKNNIPIQ
KHKHKHTLNSTWVGTNKMDIQKERERHLNIKGLGKDMGNIQRPKGVSTFGTHQDNKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYBKQEYIEDLIINYQHKMKKDIVTLKNAIIFVSKLYIEKPILLHSSYFKKNLFFVEL
KKKKHIQRTFKLPYNSSTVHIYQMKDLINNQILSNIHETLYTLVNYLTIEIFFDLNNI
IKFSLILTKDQNKNIINEHTFTGSEIYSMYNSSPYILYPFFKYSKTYLCSITGLHFMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MPSKSGRVRMPADNRLPVSASLKTSEIWKNSVGYDPYASYEEIN
KKKEKKDEDINEKAKNLFNLSRLTGITSTTIPGACTVCNHIGHLPYQCRNFISLEKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSNEGNESLLRKAKNDNLNDRFEMKEGKGMINGVMKRGDNPMGGYNTMGGNNPMGGYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEFTKI PMPQYI CYRKQTLI ENNEYLFSI IHKYNYEKNNI YI I SECLKNCPILEHCTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNNLILKLKSLKMNYMSLQDQKENNLIHLINKAIDIFLSDEMTYVEFLDEFPANLSIY
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                                                                                                                                                                                                                                          aa) fasta scores:
                                                                                                                                                                                                                                                                                                                                                 /product="guanidine nucleotide exchange factor, putative"
/protein_id="CAD51450.1"
/db_xref="GI:23504571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Weakly similar to Arabidopsis thaliana F8n16.20
protein f8n16.20 TR:Q9ZV23 (EMBL.AC005727) (332 aa) fasta
scores: E(): 2e-12, 28.763% id in 299 aa"
                                                                                                                                                                                                guanidine
                                                                                                                                                                                       /note="Similar to Plasmodium falciparum nucleotide exchange factor pfrccl (1327 E(): 9.6e-190, 97.459% id in 1338 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="hypothetical protein"
/protein_id="CAD51451.1"
/protein_id="G1:23504572"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="SPTREMBL:Q81418"
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                             complement (219. .8039)
/gene="PFE0420c"
                                                                                                          complement (219. .8039)
/gene="PFE0420c"
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/gene="PFE0425w"
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/gene="PFE0425w"
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Direct Submission
Submitted (12-JUN-1997)
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                                                                                                                                                                                                                                                                                                                                                                                        GI:37654883
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Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 69009)
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U33050.4 GI:3
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    270
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|165019 AAGAAAAAAGAATTATAGTAATAAACATATATAATAATAATAATAGTAGTGATGTCC 165078
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145
                                                                                                                                                                                                                                                                                                                                                                              GlyAlaAspTyr---GluAspTyrThrAspMetLeu-------AsnLysLeu 159
                                                                                                                                                                                                                                                        GlylleAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeuIle 105
                                                                                                                                                                                                                                                                                                                                                                                                                     AsnAsnAlaHisThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGlu 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 ArgArgArgMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAsp 269
                                                                                                                                                                                                               HisLeuAspLysGluLeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeu 85
                                                                                                                                                                                                                            AspTyrProLysLysValAspGlyLeuThrAspGluGluAspAspAspAspGlyAspGly
                                                                                                                                                                                                                                                                                                                                        LeuAspSerIleAlaAspAspGluAspAspAspValSerTyrSerSerValAspAspVal
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T->C change at nucleotide 31605, resulting in a E->G change in
YDR470C as 113, as communicated by Hartmut Wohlrab and published in
Belenkiy, R., et al. Submitted, 2000. New Sequences and Consensus
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School of Medicine, Saccharomyces Genome Database, Stanford, CA
                                                                                                                                                                                                                                                                                                                                                                                                     LeuTyrTyr------ValTyrAlaGlnIleCygTyrAgnAsnSerHis 336
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(Dases 1 to 6909)
Dietrich,F.S., Mulligan,J., Allen,E., Araujo,R., Aviles,E.,
Berno,A., Carpenter,J., Chen,E., Cherry,J.M., Chung,E., Duncan,M.,
Hunicke-Smith,S., Hyman,R., Komp,C., Lashkari,D., Lew,H., Lin,D.,
Roberts,D., Schram,S., Schroeder,M., Shogren,T., Shroff,N.,
Winant,A., Yelbon,M., Shotstein,D. and Davis,R.W.

The sequence of Saccharomyces cerevisiae chromosome IV right
SerArgProAlaAlaHisPheHisLeuSerSerArgArgArgHisGlnGlySerMetGly 289
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se Genome Database, Stanford, CA 94305-5120,
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                                                                                                                                                                                                                                                                                                              165250 AATATGAGTAATTCAAATTATGGAGTAAAATGGGAAGTAATAATAAATGATTCGACC
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                                                               290 TyrHisGlyAspMetTyrIleGlyAsnAspAsnGluArgAsnSer-------
                                                                                                                                                                                                                                                                -----TyrGlnGlyHisPheGlnThrArgAspGlyValLeuThrValThrAsnThrGly
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Submitted (02-MUG-1995) Saccharomyces Genome Database,
University School of Medicine, Stanford, CA 94305, USA
U (bases 1 to 69009)
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Residues, Lack of Direct Relation between Consensus Residues and Transmembrane Helices, Expression Patterns of the Transport Protein Genes, and Protein Protein Interactions with Other Proteins.
                                                                                                                 Direct Submission
Submitted (20-DEC-2002) Department of Genetics, Stanford University
School of Medicine, Saccharomyces Genome Database, Stanford, CA
                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (14-OCT-2003) Department of Genetics, Stanford University
School of Medicine, Saccharomyces Genome Database, Stanford, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The 5' end of this sequence contains a 1000 bp overlap with GenBank Accession Number U33007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="YDR457W; Hect-domain-containing nprotein, required for G2/M transition; similar to Rsp5p, ORF YER125w, from SwissProt Accession Number P39940, contains motifs typical of protein kinases; CAI: 0.16"
                                                                                                                                                                                          94305-5120, USA
Delection of 16 nt (GATCCTCTTGATTTT) between 1437732 - 1437747
Sequence update by submitter
(bases 1 to 69009)
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence update by submitter
On Oct 14, 2003 this sequence version replaced gi:27316972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanford DNA Sequence & Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   URL: http://genome-www.stanford.edu/e-mail: yeast-curator@genome.stanford.edu
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/evidence=not_experimental
/product="Tomlp"
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/db_xref="GI:927738"
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'db_xref="taxon:4932"
'clone="cosmid_8035"
                                                                      5 (bases 1 to 69009)
Sethuraman, A. and Dolinski, K.J.
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/chromosome="IV"
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/gene="TOM1
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FGMSLGNGSFSQVPQHLEARDFLAIIFMEDPPYEYFTSVAISNYTEVLQYLDEKYEDY
AFDDVMVVANDQLENLDPFLASPDNGSFFLERDGENSVRSGSKLCRLAALLAVTNV
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NGILTLSCLINALTFYNKSMQTETMENVQSIGKYYVSIDDDDYNIMKALTVPIIKVPATA **AKAFSDDSGENIDLRNIIIETKLNAIAFVNTIFSPPQVSSKLFELDPYAFNSLTDLIS** LSETKIPKELRTDALFTLECISLKHVWCSDIIRNLGGNISHGLLFQILRYIAKTLREA THEBIDESTWYRFYLISNLADVKPLHRSLFRAGLIPTLLEIVSIRNCPYKRTLASATH LLETRIDNSETTTEFIENDGFTMLITSVANEIDFTLAHPETWQPRYSSVYYSISFRE LAYIRSLLKLVLKELSTDSGDRIRNLIDSPILVSLKKILBNKLVPGGLTLITYTLDVVQ KVINSEPTIYPVLVEAGLIPYVIDNFPKLIGPSAELLSLLPDVVSAICLNPEGLKOVŘ EKGLINNLFDFLLDADHARILTGGDRSTEYGTDIDELARHYPDLKANIVEALCNVIRK MPSTFRNEREFLFTSPKDQKYFFHRKNEEILTDKEEHEPAYWELLDKGTMLDTFTSVL MILDLDKSDSLFKTQSRNVPYSVFKQLL.SMLKNIFTNVNIYTKELYELHWDLIPPIK KISTERQGTBGDVAANYLDTGDDDADNSTGLESPERQMEKYKKLISEBEKSIYYPQP MQAQYYKGCSSKELDERDTFPNDGLPSRIFTVLPPYPKLVNAFAKTLLQIFTKYDEP TEVFAGRILDRILETDLDDPATLSSLIHLFGIFUNEKYIYQKASHLMQRFIEYLEKSL KEPHYNTPWESKALYYYEIILAKSELHHEBLSKOVLLKPYELSMAKYCRFIPDPMKQK LFDILLRVSDISNFYARALATGRILLFYSRDELYANNIARSGTILSRLLKVIGSFQKLDK INFLESSFLLLTRRCFFTTENVDALIRASEINKSFTARPLGGGDDAVRELTTILEFEKAH VVMRSPSQFIDVLCETARFHEFDDQGALVDYSLKRFLGEKÖKVTQASSTEKSDIYERT GHHILLGEVARASEKOWTSEPANSDLPENKKOLDPSKNEVCAYMFPLKLLVELV SSYNQCKFEPLTASEKTYVAERPRFTTAINFLYRLLDKPYGTDHDKHEAKREVIG MLARSVIIGFLATVQDDRTTKTDVKLADPHMNFIRKFAIEAIIKAIRNATSSSKLLES NHLKLDMWFRITTSMVYVQAPYLRQLLDSNKVBADQYQLCKLVIDLGLPSVITFAMAS IDLNYPFSKKIFNVAVEALNTISSTRNNFSEHFKIEDHDEVEDEVDESDKEEIPDMFK NSALGMYDVEDIEEDDDDDTSLIGDDDAMAFVDSDNGFEVVFSDEDDDMGEEDADDAR SDSEENELSSEMQSSTADGTDVDYEVDDADGLIINIDQPSGDDEEMADYDANISHSSH SENEDDASMDVIEVYDDELSSGYDVDLSDYDVDESDWDSGLSSLSISDEDSESSEDEP INSTRMGDSRRRWLIAEGVELTDDSQGESEEDDRGVFRGIEHIFSNENEPLFRVHDEM RHRNHHRS INRTHFHSAMSAPSILSLINRGRRNQSNLINPIGEPTGLEQVENDISDOVTV
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SDATWHSRER IDSDFLEAI PEDIRAGILIDTEAREQKMECRIGSSADVIRADDDVSNNDE
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ELFYRLCSSKQNRNDIMNTFLFILSEGIIDQHSLEKVYNIISSRAMGHAKTTTVRQLP IFGDHNLRKKTLKLALSLSSSVMDEDGEHFSLVDLYFDKKKVPQKWRKLRFTHYTSND FKKSSQQKNNINETQTSIKKVTMTTQELCEHSLQQIFDKGMALLPAESWFDFSIKASV SDCTPLTVANQTIEILQSLIDADSRLKYFLIABHDNLIVNKANNKSRKEALPDKKLRW PLWHLFSLLDRKLITDESVLMDLLTRILQVCTKTLAVLSTSSNGKENLSKKFHLPSFD EDDLMKILSIIMLDSCTTRVFQQTLNIIYNLSKLQGCMSIFTKHLVSLAISIMSKLKS /craislation="MDHRNILDPKTLKVSQLRRVLVENDVAFPANARKPVLVKLFEEKV RRQLQSPEPASKRYFSIQKVVKSGARVADRKKTLKSKKLESSSSSEKTVKDENVETNK RRRQLGSTDNEAKWOJCERESPRKKKKRSSKANKPPESPPQSKSDGKATSADLTSEL BTVEELHKKDSSDKFRVKELPKPELPNLKVSNEFLAQLNKELASAATENYDHSIKST ALDGLSREVGTITTGMEINSELLOKFTLPSSDOAKLLKILTTVDFLYTHKRKEEBENV KDLGSLYDKMNGGPVWSSLSECLSQFEKSQAINTSATILLPLIESLMVVCRRSDLSON RNTAVKYEDAKLLDFSKTRVENLFFPFTDAHKKLLNQMIRSNPKLMSGPFALLVKNPK FKGESGVDAGGVTREMYQVLSRQMFNPDYALFLPVPSDKTTFHPNRTSGINPEHLSFF KFIGMIIGKAIRDQCFLDCHFSREVYKNILGRPVSLKDMESLDPDYYKSLVWILENDI VLDFDNKRYFFNAKLKSDNQERPKLFITVRREQVFLDSYRALFFKTNDE1KNSKLEIT IDIIETFSVETDDYGEHKVINLIEGGKDIIVTEANKQDYVKKVVEYKLQTSVKEQMD NFLVGFYALISKOLITIFDEQELELLISGLPDIDVDDWKNNTTYVNYTA°TCKEVS°FW RAVRSFDAEERAKLLQFVTGTSKVPLNGFKELSGVNGVCKFSIHRDFGSSERLPSSHT /note="similar to Saccharomyces cerevisiae hypothetical protein on chromosome XIII from GenBank Accession Number 849745, CDS number 5; CAI: 0.13" CFNQLNLPPYESYETLRGSLLLAINEGHEGFGLA" /evidence=not_experimental /product="Ydr458cp" /protein_id="AAB64934.1" /db_xref="GI:927762" complement (10786. .12777) complement (10786. .12777) gene="YDR458C" /gene="YDR458C" codon start=1

gene

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EDTSRLESSKKNIRSPKGRTRHFIANKTRGIOIMKPFTAHLETMUNGGAIFLSITOPI

LFGLWYREGRIOVGYCGHEKPLKSLAISAFPOTERVDSVLQAYRPNCLECPEHGICSS

FWNVECEPGYZERKSILETYGIIPPRYCAKORSKEKENDELWKYNSYLKKKNAQHE

CGEGRNLFESGETTTXLYDI FSHRYCAKORSKEKENDELWKYNSYLLKKKNAQHE

ETNGKREKSKSNNTYTYSTSTSKKWYTLQCHLEGBIOGYTTKYGGSLFITLPLP

ETNGKREKSKSNNTYTYRSTSKKWYTLQCHLEGBIOGYTTKYGGSLFITLSDIPNIK

ONNLWAQTKETINKEQSENIELYKZAIDKLKDVKKNKGEEPFLTTVQLRATLLSDIPNIK

COMPLAQOTKETINKEQSENIELYLLESNGEIMTCWEWKE"

/gene="YDR459C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGAAGTTGAAGACGAGGTTGACGAGTCTGATAAGGAAGAGATCCCGGATATGTTCAAA 6220
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DLSSIRIETEEPVGPSTGAETRNESEVMENINLEVQPEVKEAKEELTKISETFDNQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6437 AGTACAGCGGACGGCÁCGGATGTGGACTATGAGGTTGATGATGCAGATGGÁCTAATTATC 6496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6674 GATTGGGACTCCGGGTTATCCAGCCTATCTATTTCTGATGAAGATAGTGAAAGTAGCGAA 6733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ТутАвпАlaHisLysLysLysGlnGluArgLysSerArgSerIleAlaAspValArgAsn 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AsnTyrLeuAspGluPheAspGluPheGlnLysGlu------TyrGlu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluAspAspAspAsp-----124
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                                                                                                                                                                                                                                           /gene="YDR459C"
/note="similar to Saccharomyces cerevisiae hypothetical
protein from PIR Accession Number S51289; CAI: 0.12"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----Glu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATATTGACCAGCCCTCAGGAGATGATGAAGAAATGGCAGACTATGATGCTAACATTAGC
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                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
DB:
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013 CAAAGCAACCTAATAAATCCACTAGGGCCTACAGGTTGGAACAAGTGGAGAACGATATT 7072
                                                                                                                                         ------GGTGAGAGTGAAGAAGAT 6838
                                                                                                                                                                                                                            LeuTyrTyrValTyrAlaGlnIleCysTyrAsnAsnSerHisAspGlnAsnGlyPheIle 342
                                                                                                                                                                                                                                                                                    343 ValPheGlnGly-----AspThrProPheLeuGlnCysLeuAsnThrValProThrAsn 360
                                                     264 LysAlaArg---SerGluAspSerArgProAlaAlaHisPheHisLeuSerSerArgArg 282
                                                                                                            ArgHisGlnGlySerMetGlyTyrHisGlyAspMetTyrIleGlyAsnAspAsnGluArg 302
244 ProAlaProLeuHisHisArgArgArgMetHisSerArgHisArgHisLeuLeuValArg 263
                                                                                                                                                                                                                                                                                                                                                                                                     -----ArgAsnGluArgIleHisLeu 384
                                                                                                                                                                                      AsnSerTyrGlnGlyHisPheGlnThrArgAspGlyValLeuThrValThrAsnThrGly
                                                                                                                                                                                                                                                                                                                                            361 MetProHisLysValHisThrCysHisThrSerGlyLeuIleHisLeuGlu-----
                                                                                6794 GGCGTGGAGCTAACTGACGACTCGCAA--
                                                                                                                                          TCGGAAGTT 7141
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completed: September 15, 2004, 10:23:34 e: 7208 secs Search co Job time

cDNA enco Polynucle Human EDA

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Gene sequ Human cDN Kaposi's Nucleotid

RRP3 telo Drosophil

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KSHV LUR KSHV long

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Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithalial morphogenesis; cell-matrix adhesion; x-linked anhidrotic (hypohidrotic) ectodermal dysplasia; x-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder; sparse hair; sweat gland aberration; endocoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; TNFv2; obesity-linked insulin resistance; gene; ds.
                Abaa70099
Ab106443
Ab106443
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Ab1060443
Ab10609
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Ab25257
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Ab21276
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/product= "TNFv1"
/note= "Tumour necrosis factor variant 1"
634. .1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/note= "Specifically claimed in claim 22"
634. .789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding tumour necrosis factor variant 2 (TNFv2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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ABL03529
AAT27052
                                                                                                                                                                                                                                                                                                                   ABK43159
ADC46185
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ACC60802
                                                                                                                       ACC57577
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790. .1860
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RESULT 1
ABK11680
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                                 Command line parameters:
-MODEL=frame+ pln.model -DEV=xlp
-MODEL=frame+ pln.model -DEV=xlp
-MODEL=frame+ pln.model -DEV=xlp
-Cgn2_1/USPTO_spool_p/US09813329/runat_13092004_102752_21656/app_query.fasta_1.583
-DB=N Geneseq_29Jan04 -OFWT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MINE-0 -AMXIEN=15
-MODE=LOCAL -OUTFWT=pco -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=2000000000
-USER=US09813329_@CGN 1 1 885_@runat_13092004_102752_21656 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGG_SCORES=0 -MAXIT -DSPBADCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Abk11679 DNA encod
Abk11678 DNA encod
Abl21473 Drosophil
Abse4139 Mouse cDN
Abl15995 Drosophil
Abd76511 C. albica
                                                                                                                                        (without alignments)
2740.557 Million cell updates/sec
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                                                                                                                                                                                                                            ......DRNAVLREGNNRSYFGIFKV 409
                                                                                                                     September 15, 2004, 02:17:51 ; Search time 634 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                      3373863 segs, 2124099041 residues
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated tumour necrosis factor polypeptide

(TNF) The polypeptide and polynucleotide are useful in controlling

agriculturally important peets, particularly by modifying the growth,

feeding and/or reproduction of crop-damaging insects or insects of farm

animals. The polypeptide and polynucleotide are useful for modulating

cepithehial morphogenesis, cell-matrix adhesion in files and mammals. Thus

the polypeptide and polynucleotide may be useful for recating,

ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal

dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal

dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal

ike disorders, e.g. sparse hair, abnormal or missing teeth or sweat

gland aberrations in animals (e.g. insects and potentially humans),

endocoxic shock, inflammation, haemorrhagic necrosis of tumours,

cytotoxicity and obesity-linked insulin resistance, all of which involve

TNF molecules. This sequence encodes the drosophila melanogaster tumour

recosis factor variant 2 (TNFv2) protein, described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    693
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                                                                                                                                                                                                                                                         New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals.
                                                                                                                                                                                                     ΑÞ.
                                                                                                                                                                                                      Bowen
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RAMANATHAN C S
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(first entry)

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                                                                                   Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasis; sparse half, sweat gland aberration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxic shock; inflammation; obesity-linked insulin resistance; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                       claim 18"
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1. .1218
//taga d
//tage = "Specifically claimed in claim 1
1. .156
**Ataga a
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                                                     tumour necrosis factor variant 1 (TNFv1)
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/label= mature_TNFv1
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1. .1221
/*tag= b
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480 180 240

Claim 2; Fig 2A-B; 119pp; English.

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753 274 813 294 314

933

TACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTTCAAACGCGGATGGC

g

Sequence 1221 BP; 349 A; 323 C; 312 G; 237 T; 0 U; 0 Other,

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240 100 300 120 360 140 420 160

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'product= "TNFv1"

misc_difference

sig_peptide

mat_peptide

melanogaster.

Drosophila

__ag=_a 157. .1218 /*tag=_c /lahr

20-MAR-2001; 2001US-00813329 21-MAR-2000; 2000US-0190816P

US2002012968-A1

31-JAN-2002

CHEN J.
RAMANATHAN C &
XIAO H.
GUAN B.

CARROLL P M.

CARR/)

(CHEN/) CHEN J.
(RAMA/) RAMANATHAN C
(XIAO/) XIAO H.
(GUAN/) GUAN B.

Chen J,

ΡΜ,

Carroll

WPI; 2002-195121/25

us-09-813-329-6.rng

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The invention describes an isolated tumour necrosis factor polypeptide (TNF). The polypeptide and polymucleotide are useful in controlling agriculturally important peets, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polymucleotide are useful for modulating captupential and polymucleotide may be useful for modulating the polypeptide and polymucleotide may be useful for treating the polypeptide and polymucleotide may be useful for treating crop-damaging ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal dysplasial and X-linked anhidrotic (hypohidrotic) ectodermal dysplasial and X-linked anhidrotic (hypohidrotic) ectodermal dysplasial its disorders, e.g. sparse hair abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), endocatic shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obseity-linked insulin resistance, all of which involve TNF molecules. This sequence encodes the drosophila melanogaster tumour necrosis factor (TNF) protein, described in the invention
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                                      New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm
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        Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; pelithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder; sparse hair; sweat gland aberration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; obck; inflammation; obesity-linked insulin resistance; gene; ds.
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product= "TNF"
note= "Tumour necrosis factor"
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/note= "Specifically claimed
652. .1881
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                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    v Zis-SR nucleic acid molecules and polypeptides, useful for restoring increasing the secretory properties of a cell, or for treating leases or conditions associated with a loss of function, e.g. diabetes
                                   GACGGTGACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACAACAACAACA
                                                                                                                                                                  rValProThrAsnMetProHislysValHisThrCysHisThrSerGlyLeulleHisLe
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                                                                      uThrValThrAsnThrGlyLeuTyrTyrValTyrAlaGlnIleCysTyrAsnAsnSerHi
                                                                                                                     sAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGlnCysLeuAsnTh
                                                                                                                                 CGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCATTCCTGCAGTGCTTGAACAC
                                                                                                                                                                                    GGTGCCCACCAACATGCCACATAAGGTGCACACTGCCACACGAGTGGTCGTGATCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; ss; gene; Zis-SR; neuroendocrine phenotype; diabetes; Parkinson's disease; Zinc finger splicing with extended Ser-Arg domain; secretory pathway; zinc finger protein.
                                                                                                                                                                                                                                                                                         1043 GGAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTG 1004
                                                                                                                                                                                                                                                                   gGluGlyAsnAsnArgSerTyrPheGlyIlePheLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse cDNA encoding Zis-SR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Zis-SR"
                                                                                                                                                                                                                                                                                                                                         ABS54139 standard; cDNA; 2616 BP
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stringency contraction to the 218-5K mucletc actd. Also included are an isolated polypeptide involved in the formation of secretory granules in cells comprising the amino acid sequence spanning amino acids 243-310 of the Zis-SR protein, restoring the neurosandocrine differentiation of a cell using the mucleic acid molecule or polypeptide cited above, identifying a gene and/or protein involved in inducing regulated secretion comprising a comparison at the molecular level of a secretion-defective cell in the absence of the conditions of the secretion-defective cell line in the absence of the conditions cited. Also included are modulating the secretion is restored, and the secretion-defective cell line in the absence of the conditions cited. Also included are modulating the secretion in a cell comprising an assassment of a biological activity of Zis-SR and an assay to identify a modulator of regulated secretion in a cell comprising an in assessment of a biological activity of Zis-SR its part or derivative is measurably different in the presence of the candidate compound as compared in its absence. The nucleic acid molecules or properties of a cell, for restoring or increasing the secretory compound as compared in its absence. The nucleic acid molecules or properties of a cell, for restoring or increasing the secretory clong term therapies to treat diseases or conditions associated with a long term therapies to treat diseases or conditions associated with a certain certain centain cells as an also be used to locate gene regions associated with a defect in the regulated secretory pathways in cells. The nucleic acid defect in the regulated secretory pathways in cells. The nucleic acid defect in the regulated secretory pathways in cells. The nucleic acid defect in the regulated secretory pathways in cells. The nucleic acid defect in the regulated secretory pathways in cells. The nucleic acid defect in the regulated secretory pathways in cells. The nucleic acid defect in the regulated secretory pathways and the secreto present sequence encodes mouse Zis-SR (zinc finger splicing Ser-Arg domain) diseases. The with extended

542 G; 782 T; 0 U; 0 Other; Sequence 2616 BP; 834 A; 458 C;

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                                                                                                                                                                                                                                                                                                                                                                               AspGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGly 113
                                                                                                                                          rrrecraggagaaccagcreraacagareregreeagaaagacaacreaggecaagare 154
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                                                                                                                 PheProAlaLysAlaThrSerThrAlaThrAlaGlnArgArgThrArgGlnLeuIlePro 39
                                                                                                                                                                                                                      AlaLeuThrIleTrpGlnThrThrArgValSerHisLeuAspLysGluLeuLysSerLeu 74
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            Matches:
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Mismatches:
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AspAspGluAspAspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGlu 150

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The invention relates to an isolated nucleic acid molecule, Zis-SR, encoding a protein involved in the secretory pathway in a cell(or its homologue or variant) or nucleic acid molecules that hybridise under high

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                                     GluThrThrAlaGluGlyGluGlyGluThrAspSerAlaSerAlaSerAsnAspAsp 190
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AspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHisThrGlyThrThrProThrSer 170
                                                                                              ArgSerIleAlaAspValArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeu 230
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GlylleAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeuIle 105

98

HisLeuAspLysGluLeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeu 85

99

Length:
Matches:
Conservative:
Mismatches:
Indels:

0.0501 145.50 37.40% 23.66% 6.73%

1445 CACATTAGGAATGCCGCACCAGCATCAGCGAATGCGTTGCCTCGGATGAGGACAAGCAG

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AspTyrProLysLysValAspGlyLeuThrAspGluGluAspAspAspAspGlyAspGly

126 LeuAspSerIleAlaAspAspGluAspAspAspValSerTyrSerSerValAspAspVal 145

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.610 AGTGCCGAGTGTGATGACTTTACAACCCTGTCGCAACTAAATGAACAACAACAACAGGCGCTG 1669

146 GlyAlaAspTyrGluAspTyrThrAspMet-----LeuAsnLysLeuAsnAsnAlaHis 163

ThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAspSerAla 183

164

Drosophila melanogaster expressed polynucleotide SEQ ID NO 42467.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-00614150.
                                      pharmaceutical; gene; ss.
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P-PSDB; ABB71892.
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Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases.
                                           SerIleAlaAspValArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGln
                                                                                                                                                                                                                                                                                                                                                                                  2075 AAGTCCGCTTCCACTCCGGCTCCGCCGACAAATCGGATGCCATCTCGGCCGCCTCGCTT
                          SerSerAlaSerAsnAspAspAsnValPheAspAspPheThrSerTyrAsnAlaHisLys
                                                                                                                                                                                            GluLysSerSerAsnGluAlaThrSerLysGluSerProAlaPro--------
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1958 GGCGATGCAACAGCAATTGGCACATTCTTCAACAATCTGCTGTCGCATTCCAATGCAGGT
                                                                                                                                                                                                                                                                                                        tHisSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAspSerArgProAl
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1670 TCAGCGGCATTGAAATTGCCCACAACAACAGCAGCATCATCAGGC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegeneration; cell death; ss
                                                                                 LysLysGlnGluArg-----
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P-PSDB; ABG93245.
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This invention describes a newest neutron acre representing a symmetric cesistant yeast or fungi, identifying, or obtaining and identifying Baxresistant yeast or fungi, identifying, or obtaining and identifying a candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the inhibitor sequences of Bax-induced cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vascincion have cytostatic, fungicide; immunosuppressive, virucide and vascincian and compositions, antisense molecules and antibodies are useful as medicaments or in preparing a medicament for treating, preventing and/or alterviating diseases associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds or publicating a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunishing against yeast or inference in the composition of the mammals. The vaccine is useful for immunishing against yeast or inference in the section of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polynucleotide associated with the Bax gene described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                            describes a novel nucleic acid representing a synthetic
                   Claim 36; Fig 2; 344pp; English.
\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset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Sequence 1287 BP; 490 A; 237 C; 253 G; 307 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                    316 TTAGCAGGCAAAGAATTACCAAAAGTTTCTAAACAGTTGGAATCCATTATTGATGAAGTG 375
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                                                                                                                                                                                                                                                                                                                                                                           GAAAATCAAGAAAAGGAAAGCAAACCAAGAAACTCATCATCTGATAGTGAAGACTCTTCA 435
                                                                                                                                                                                                                                                                                                                                                                                                        98 LysGluTyrGluAsnAlaLeuIleAspTyrProLysLys------ValAspGlyLeu 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThraspGluGluaspaspaspAspGlyaspGlyLeuAspSerIleAlaaspAspGluasp 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 AspAspValSerTyrSerSerValAsp---AspValGlyAlaAspTyrGluAspTyrThr 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspMetLeuAsn---LysLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThr 172
                                                                                                                                                                                                                                                                                ...----LysSerLeuLysArgValValAspAsnLeu 81
                                                                                                                                                                                                                                                                                                                                              82 GlnGlnArg------LeuGlyIleAsnTyrLeuAspGluPheAspGluPheGln 97
                                                                                                                                                     GinteulleProteuVal --- LeuGlyPheileGlyLeuGlyLeuValValAlaileLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaLeuThrIleTrpGlnThrThrArgValSerHisLeuAspLysGluLeu----
              1287
76
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137
86
              Length:
Matches:
Conservative:
Mismatches:
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                                                                                          Gaps:
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141.00
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193 PheAspAspPheThrSerTyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSer 212

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                                                                                                                                                                                        GGAGAAAAGGCTAGTGAAAATTATTACAAGTCAGAGGTAAAGATTTCACAAAGAATAAA 1212
                                                                                                                                                                                                                                                                                                         ------GGTAGTATCACT 1254
                  --GluGlnAsnIleGlnGly 225
GACTCTGATTCAAGTTCTGATTCCGACTCCAGCTCCAGCTCTGATTCCGACTCCAGCTCC 795
                                                                                           246 ProLeuHisHisArgArgArgMetHisSerArg-----HisArgHisLeuLeuValArg 263
                                                                                                                                   -------AspSerArgProAlaAla 274
                                                                                                                                                                      ----HisPheHisLeuSerSerArgArgArg 283
                                                                                                                                                                                                            -----HisGlnGlySerMetGlyTyrHis 291
                                                                                                                                                                                                                                                                                     Asn-----GluArgAsnSerTyrGlnGlyHisPheGlnThrArgAspGlyValLeuThr 317
                                                                 Erythropoietin, EPO, G-CSF; granulocyte colony stimulating factor; wobble; codon altered gene; shuffling; modification; vaccine; insulin; peptide hormone; growth factor; cytokine; interferon; interleukin; leukaemia inhibitory factor; oncostatin M; transcription activator; expression activator; infectious organism; ds.
                                   796 AGCTCTGATTCCGATTCAGACTCAGATTCTGATAGTGACAGTGACGACAATTCCTCAGAA
                                                      226 AsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThrSerLysGluSerProAla
                                                                                                             913 CAACCAGAAGACAAGAAAAGAAAGCACAGATGATATCAAAGAAAAAAACCAGTTAAA
                                                                                                                                                                                                                                                 ---TyrileGlyAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV codon altered env nucleotide sequence #2.
                                                                                                                                                                                                                                                                                                       AATAAAATGAAGAGAGGAAGTTATAAAGGA
                                                                                                                                 LysAlaArgSerGlu------
                                                                                                                                                                                                                                               GlyAspMet-----
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TTAGCT---AGTGGGTCCTAT 1272
                                                                                                                                                                                                                                                                                                                        ValThrAsnThrGlyLeuTyr 324
                213 IleAlaAspValArgAsnGlu-
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99US-0117729P.
99US-0118813P.
99US-0141049P.
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                                                                                                                                                                                                                                                                                                                                                                                 AAA29550 standard; DNA; 567
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAXY-) MAXYGEN INC
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comprising providing a NA sequence (NA1) which encodes a polypeptide (PI), providing a NA sequence (NA1) which encodes a polypeptide (PI), providing codon altered NA sequences, each encoding P1 or a modified form of it, and recombining the codon altered NA sequences to produce a target codon altered NA which encodes a second protein. The method of the invention can be used for recombining codon-altered libraries of mucleic acids to produce new proteins, which have improvements in a desirable characteristic. Target nucleic acids include those coding for therapeutic proteins such as erythropoietin (BPO), insulin, peptide hormones, growth factors, cytokines, interferons, interleukina, leukaemia inhibitory factor, and oncostatin M, as well as transcription and expression activators and proteins from infectious coganisms for use as vaccines. The method can also be used to produce attenuated viruses which have reduced rates of reversion to wild type.

The present sequence represents an HIV codon altered env nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 AspMetLeuAsnLysLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThrThr 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 AspAspPheThrSerTyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 AlaGluGlyGluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 SerSerAsnGluAlaThrSerLysGluSerProAlaPro-LeuHisHisArgArgArgMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 AspAspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGluAspTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AlaAspValArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLys
Novel methods for recombining codon-altered libraries of nucleic used to produce new proteins and new vectors with reduced rates o reversion to wild type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 567 BP; 32 A; 129 C; 222 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGCCGCCGACGACGACGACGACGACGACGA 18
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Matches:
Conservative:
Mismatches:
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                                                                                                              English
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46.24%
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                                                                                                        Example; Fig 18A; 92pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and polyclonal antisors or a monoclonal antisody raised to infection. (I) and polyclonal antisors or a monoclonal antisody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they can reduce or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the condum chromosome 2 and the subsequent identification of proteins can process hampered by the complexity of the parasitic lifecycle, and process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistence to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA7078 to AAA70287 and AAB1814 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the
                                                                                                                                                                       Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:232
                                                                                                                                                                                                                     Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide; ds.
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and in the
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                           AAA70099 standard; DNA; 3579
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CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VENTER J C.
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2269 AGT------TTGAAAACGAAAAATTATTATCCACATAATATGACATTTGGACAA 2316
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2167 AAAGAAGATAACAAAGAAAAAGACAAAGAAGATGAC-------AAAGAA 2208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 PheAspAspPheThrSerTyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSer 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 IlealaAspValArgAsnGluGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGlu 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 AspMetTyrlleGly-----AsnAspAsnGluArgAsnSerTyrGlnGlyHisPheGln 310
                                                                                                                                                                                                                                                                                             ------AspAspAspAspGlyAspGlyLeuAspSerIleAlaAspAspGluAsp 134
                                                                                                                                                                                                                                                                                                                                                                                                            135 AspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGluAspTyrThrAsp 154
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                                                       88 AsnTyrLeuAspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeu-----
                                                                                                              105 -----IleAspTyrProLysLysValAspGlyLeuThrAspGluGlu------
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ABL06443 standard; cDNA; 6240 BP

68 AspiysGluLeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeuGlyIle 87

US-09-813-329-6 (1-409) x AAA70099 (1-3579)

--AsnValPheAspAspPhe 196

793

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208 ArgLysSerArgSerIleAlaAsp-----ValArgAsnGluGlu 220
                                                                                                                                                                                                                                                                                           -----LysGluSerProAlaProLeuHisHisArgArgArgMetHisSerArgHisArg 258
                                                                                                                                                                                                                                                                                                                                                                  259 HisLeuLeuValArgLysAlaArgSerGluAspSerArgProAlaAlaHisPheHisLeu 278
                                                                                                                                                                                                                                                                                                                                                                                                       854 CGGCGCAGGGTGAAACCCTTTAGTTCCGAGGACAGTGATGATGACGACGCTAGCAAACGC 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; EDA1-II; X-linked hypohidrotic ectodermal dysplasia; XLHED;
DL receptor; DL gene; downless gene; ectodermal dysplasia;
hair follicle growth; tooth growth; endocrine sweat gland development;
mammary epithelial tissue growth; breast epithelium; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a purified hypohidrotic ectodermal dysplasias protein (I) that promotes the development of hair follicles. (I) is a promoter of hair follicle growth and tooth growth. (I) is useful for the development of hair follicles. (I) is also useful for commercial and clinical diagnostic testing for ectodermal dysplasia (ED). (I) is also useful as a stimulant for hair and tooth growth, for stimulating
                                                                                                                                                                      794 GCCCAAAAGCGCAAACCGGCAACTACCTCCGCAGCAACTCGCACAGCACAGCAG
                                  --TyrAsnAlaHisLysLysGlnGlu
                                                                                                       TCCAGCAGCAGCAGCAGGAGGAGGAGGACTATAGACCCAAGCGGACGCCCAGGCC
                                                                                                                                                                                                                  GlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel purified hypohidrotic ectodermal dysplasias protein, useful for promoting the development of hair follicles and tooth growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                         279 SerSerArgArgArgHisGlnGlySerMetGlyTyr 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  914 TGCGCTACTCGTCGCAAGGGTGCTGCCGTTAGCTAC 949
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AlaSerSerAlaSerAsnAspAsp.
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98US-0112366P.
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P-PSDB; ABB09082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811.
                                                                                                                   developmental biology; cell signalling; insecticide;
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endocrine sweat gland development in individuals from whom the normal sweating mechanism is compromised by disease or surgery, for stimulating the growth of mammary epithelial tissue, either for reconstructing or cosmetic purposes, and for promoting or maintaining differentiation of breast epithelium. (I) is also useful for functional analysis, antibody production and patient therapy. ABL51009 to ABL51122 and ABB09082 to ABB09090 represent sequences used in the exemplification of the present
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                                                                                                                                                                           AGAIGGIGCACGCIGACAICTCC-----ATCAACAIGAGCAAGCACCACGITCIITG
---ArgProAl
                                       a-AlaHisPheHisLeuSerSerArgArgArgHisGlnGlySer---MetGlyTyrHisG
                                                     -----AsnSerTyrGlnG
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                    CCCCTGGCCTCCAGGGACCTTCTGGTGCTGATAAAGCTGGAACTCGAGAAACCAGC
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The invention relates to a method of increasing or decreasing one or more of hair follicle development, tooth development, or sweat gland development, in a tissue, involves altering ectodermal dysplasia (EDA1) isoform II (EDA1-II) activity in the tissue. The method is useful for increasing or decreasing hair follicle development, tooth development or sweat gland development, in a tissue of a patient suffering from an ectodermal disease such as X-linked hypohidrotic ectodermal dysplasia (KLHED), autosomal recessive hypohidrotic ectodermal dysplasia (HED) or alopecia. The method is useful for decreasing hair follicle development in a subject suffering from hirsuitism. The method is also useful for treating preast cancer and ectopic teeth, burns and trauma of skin due to
            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating preast cancer and ectopic teeth, burns and trauma of skin due to surgery. The present sequence represents DNA encoding human EDA1-II
Increasing or decreasing hair follicle development, tooth development, sweat gland development, in a tissue, involves modulating ectodermal dysplasia protein isoform II activity in the tissue.
                                                                                                               Example 1; Page 59-60; 102pp; English
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Sequence 1176 BP; 271 A; 354 C; 335 G; 216 T; 0 U; 0 Other;

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------CTAGAGTIGCGCTCGGA 200
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(BAYU) BAYLOR COLLEGE MEDICINE.

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Trccaggaacaactgttatgggaccacctggtcctccaggtcctcctggtcctcaaggac
                        rSerAsnGluAlaThrSerLysGluSerProAlaProLeuHisHisArgArgArgMetHi
                                                   CAGGACCCCCAGGACCTCCAGGACCCCCAGGAATTCCAGGGATTCCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                     924 CCCTGGCCTCCAGGGACCTTCTGGTGCTGATAAAGCTGGAACTCGAGAAAACCAGC
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                                                                                                                                                                                                                             The present invention describes a purified hypohidrotic ectodermal dysplasias protein (1) that promotes the development of hair follicles. (1) is a promoter of hair follicle growth and tooch growth. (1) is useful for the development of hair follicles (1) is also useful for commercial and clinical diagnostic testing for ectodermal dysplasia (ED). (1) is also useful as a stimulant for hair and tooth growth, for stimulating endocrine sweat gland development in individuals from whom the normal sweating mechanism is compromised by disease or surgery, for stimulating the growth of mammary epithelial tissue, either for reconstructing or cosmetic purposes, and for promoting or maintaining differentiation of breast epithelium. (1) is also useful for functional analysis, antibody production and patient therapy. ABL51009 to ABL51122 and ABB0908 to
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P-PSDB; ABB09082.
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The invention relates to a method of increasing or decreasing one or more of hair follicle development, tooth development, or sweat gland development, in a tissue, involves altering ectodermal dysplasia (BDA1) isoform II [BDA1-II] activity in the tissue. The method is useful for increasing or decreasing hair follicle development, tooth development or sweat gland development, in a tissue of a patient suffering from an ectodermal disease such as X-linked hypohidrotic ectodermal dysplasia (HBD) or allopedia. The method is useful for decreasing hair follicle development in a subject suffering from hirsutism. The method is also useful for treating breast cancer and ectopic teeth, burns and trauma of skin due to surgery. The present sequence represents CDNA encoding human BDA1-II
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                                                                                                                                                                                                                                                               Increasing or decreasing hair follicle development, tooth development, sweat gland development, in a tissue, involves modulating ectodermal dysplasia protein isoform II activity in the tissue.
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98US-0112366P.
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P-PSDB; ABO01928.
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Best Local Similarity:
Query Match:
                                                                09-JUL-1998;
15-DEC-1998;
29-JUN-1999;
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146 yAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHisThrGly--
                                 ----AGTCACCTTGGGCA
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RESULT 1
US-09-342-681C-14
; Sequence 14, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; CURRENT APPLICATION NUMBER: 05/09/342,681C
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/12/36
; PRIOR APPLICATION NUMBER: 60/112,366
; REACH FILING DATE: 1998-12-15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO. 14
LENGTH: 1176
                                  Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 37, Appl
Sequence 37, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 1481, Ap
Sequence 25, Appl
Sequence 32, Appl
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US-08-971-089-3
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US-09-105-343A-1
US-09-103-840A-2
US-09-103-840A-1
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-DB=ISBudd_Patents NA -QFMT=fastap -SUFFIX=rni -MIÑMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-NODEL-COAL. -OUTFWT=PROFONE - THR AND -LARASIZE=200000000
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-NO MMAP -LARGEQÜERY -NEG SCORES=0 -WALT -NSPBLCOK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                          September 15, 2004, 06:59:38 ; Search time 103 Seconds
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                         - nucleic search, using frame_plus_p2n model
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US-09-342-681C-1
US-09-342-636-1
US-08-728-323A-1
US-09-298-568-1
US-09-298-568-1
US-09-399-1
US-08-399-1
US-08-377-663A-20
US-09-230-371A-20
US-08-331-27-080-27
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US-08-345-294-27
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Query Match

Result

Database :

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Searched:

Scoring table:

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131 AspAspGluAspAspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGlu 150
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OTHER INFORMATION: Incyte ID No. 6673549 238877.11
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PREL PROGRAM
LENGTH: 3034
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Patent No. 6673549
Patent No. 6731549
Patent No. 6731549
Patent No. 6731549
Patent No. 6731549
APPLICANT: Purness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTOR: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
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  yAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHisThrGly-- 165
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864 TTCCAGGAACAACTGTTATGGGACCACCTGGTCCTCCAGGTCCTCCTGGTCCTCAAGGAC 923
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TYPE: DNA (CREANISM: Kaposi's sarcoma-associated herpesvirus US-09-298-568-1
     US-09-813-329-6 (1-409) x US-08-728-323A-1 (1-3489)
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Patent No. 6322792
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GlnGluLysSerSerAsnGluAlaThrSerLysGluSerProAlaProLeuHisHisArg 250
                       268 -----GluAspSerArgProAlaAlaHisPheHisLeuSerSerArgArgArgHisGln 285
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                                                                                                      932 TCTAGGICCAGGICCGITCAAGAAGITCTICCAGITCGCAGICAAGAICTCGITCCAGI 991
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Bobenzky, Roy A.
APPLICANT: Moore, Patrick S.
ITILE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Brooding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                   251 ArgArgMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSer
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 1212-278-0400
TELEFAX: 212-278-0400
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STREET: 1185 Avenue of the Americas
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Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STATE: New York
COUNTRY: U.S.A.
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Best Local Similarity:
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MOLECULE TYPE:
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US-08-728-323A-1
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APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                             111 ValAspGlyLeuThrAspGluGluAspAspAspAspGlyAspGlyLeuAspSerIleAla
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                                                                                         US-09-813-329-6 (1-409) x US-09-298-568-1 (1-3489)
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Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or E
TITLE OF INVENTION: Methods to Inhibit or E
TITLE REPERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.0
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                                 Percent Similarity:
Best Local Similarity:
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                                            sarcoma-associated herpesvirus
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LENGTH: 3489
TYPE: DNA
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US-09-410-399-1
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20505 GAGCCAC---AACAGCAGGAGCCACAAGAAGCCACAGAGGAGCCACAGAGAGCAGGAG
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             ---GluLeuGlnGlu-LysSer---SerAsnGluAlaTh 239
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APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  20448 CAGGAGCCACAGCAGAGCCACAGCAGCAGGAGCCAC 20409
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
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Matches:
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; Sequence 20, Application US/08757669A
Patent No. 6183751;
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
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nucleic acid
EDNESS: double
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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: U.S.A.
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Best Local Similarity:
Query Match:
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US-08-757-669A-20
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STREET: 118
CITY: New Y
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      POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                               STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                         ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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35.47%
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TITLE OF INVENTION: POL-
TITLE OF INVENTION: HERI
WHMER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DI
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APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
FILLE REPERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT APPLICATION NUMBER: PCT/US97/13346
PRIOR PPLICATION NUMBER: PCT/US97/13346
                                 AspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLys 110
                                                                                                 111 ValAspGlyLeuThrAspGluGluAspAspAspAspGlyAspGlyLeuAspSerIleAla 130
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US-09-813-329-6 (1-409) x US-08-757-669A-20 (1-32207)
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US-09-230-371A-20/c
; Sequence 20, Application US/09230371A
; Patent No. 6348586
; Patent Temperation;
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SOFTWARE: Patentin Ve
SEQ ID NO 20
LENGTH: 32207
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Patent No. 569866
GENERAL INFORMATION:
APPLICANT: Stage, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20448 CAGGAGCCACAGCAGAGCCACAGCAGCAGGAGCCAC 20409
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     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                       US-09-813-329-6 (1-409) x US-09-230-371A-20 (1-32207)
                              133.00
35.47%
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                                                         Percent Similarity:
Best Local Similarity:
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177 GluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnValPheAspAspPhe 196
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Patent No. 5916752
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SINGENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Cloppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/938,534 FILING DATE: 55-SEP-1997 CLASSIFICATION: 536 PROOR APPLICATION DATA: APPLICATION DATA: PILING DATE: 08/431,080 PILING DATE: 08/431,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
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:083 TTTGATATGCCGTTTTATGAA 2103
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Arno
STREET: P.O. Bo
CITY: Houston
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73
48
126
120
                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILLING DATE: CONCURRENTLY Herewith
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Conservative:
Migmatches:
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                                                                                                                                          FILING DATE: CONCURTENTLY Herewith CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CTASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: 32,165
REGISTRATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELEPAX: 70,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4599 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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32.97%
19.89%
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               ZIP: 77210
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
DB:
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US-08-431-080-27
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                                                                                                                                                                                               216 ValArgAsnGluGluGluGlnAsn-----IleGln 224
                                                                                                                                                                                                                                                                                                                  GlyAsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThrSerLysGluSerPro 244
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                                                                      ThrSerTyr---AsnAlaHisLysLysLysGlnGluArgLysSerArgSerIleAlaAsp
                                                                                                                               618 ATTAGTTTTGGTAATGGTAATGAAGGCTATAACGAGGATATAGGTGAAGAAGTCTTGGAT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Parker, David L.
RRGIGSTRATION NUMBER: 32.165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-Jun-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
FILING DATE: «Unknown»
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gottschling, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                       2083 TTTGATATGCCGTTTTATGAA 2103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/09345294; Patent No. 6387619; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4599 base pairs
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STRANDEDNESS: single
                                                                       TOPOLOGY: linear
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1618 ATTAGTITITGGTAATGGTAATGAAGGCTATAACGAGGATATAGGTGAAGAAGTCTTGGAT 1677
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Mismatches:
Indels:
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           ATTORNEY/AGENT INF....

ATTORNEY/AGENT INF....

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REGISTRATION NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEFAX: (713) 789-2679

TELEFAX: 79-0924

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERICATICS:
ILENGTH: 4599 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                   Length:
Matches:
 SN 08/326,781
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APPLICATION NUMBER:
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1903 GAAGAACAAAACATTGTTTCTGAGCTACAAAATGACGACGAACTCTCATTCGATGGTAGT 1962
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                                                                                                                                                                                                                                                                                                                                           2023 TACAATCAAGAAAACGGATATGATGAAGAAGATGACGAAGAAGATGAAATAATGTCTGAT 2082
                                                                                                                                                265 AlaArgSerGluAspSerArgProAlaAlaHisPheHisLeuSerSerArgArgAfis 284
                                                                                                                                                                                                                                                                                                 285 GlnGlySerMetGlyTyr-------HisGlyAspMetTyrlleGlyAsnAsp 299
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245 AlaProLeuHisHisArgArgArgMetHisSerArgHisArgHisLeuLeuValArgLys
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TITLE OF INVENTION: Telomerase Compositions and Methods NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
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0y 300 AsnGluArgAsn	Oy 346 GlyAspThrProPheLeuGln 352	Craig A. Rosen Steven C. Barabh Michael R. Farnon Michael R. Farnon TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5256 CORRESPONDENCE ADDRESS: STREET: 9410 Key West Avenue CITY: Rockville COUNTY: Rockville COUNTY: Rockville COUNTY: Anyland COUNTY: Anyland COUNTY: Anyland COUNTY: Anyland COUNTY: Anyland COUNTY: 20850	EADABLE FORM: M TYPE Diskette TER: HP VOCTRA LING SYSTEM: MSI ARE: ASCII TEXT PLICATION DATA: CATION NUMBER: U IFICATION OCT-IFICATION OF CATION ICATION DATA: CATION NUMBER: GATION NUMBER: GATION NUMBER: CATION NUMBER: GATION NUMB	FILING DATE: January 3, 1997 ATTORNEY AGENT INFORMATION: NAME: WAT'S Hyman REGISTRATION NUMBER: 46,789 REFERENCE/DOCKET NUMBER: PB248P1 TELECOMMUNICATION INFORMATION: TELEFAX: (301) 309-8439 INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 4522 base pairs TYPE: nucleic acid STRANDEDNESS: double STRANDEDNESS: double TOPOLOGY: linear TOPOLOGY: linear	Alignment Scores: 0.00187 Length: 4522 Pred. No.: 128.50 Matches: 73 Percent Similarity: 30.25\$ Conservative: 48 Best Local Similarity: 18.25\$ Mismatches: 120 Query Match: 4.9\$ Gaps: 13
## SEQUENCE DESCRIPTION: SEQ ID NO: 27: ### Alignment Scores: Pred. No.: 0.0017 Length: 4599	Qy 69 LysGluLeuLysSerLeuLysArgValValAspAsnLeuGInGInArgLeuGlyIleAsn 88 Db 1114 AAAAAAGTAAACTTATACAAAGGCAAATAGACAATGACGACGGGGGC	OY 124 AspGlyLeuAspSerIleAlaAspAspGluAspAspValSerTyrSerSerValAsp 143	161 ASDALAHISThrGlyThrThrProThrSerGluThrThrAlaGlu	197 ThrSetTyrAsnAlaHisLysLysGlnGluArgLysSerArgSerIleAlaAsp 215	Qy 265 AlaArgSerGluAspSerArgProAlaAlaHisPheHisLeuSerSerArgArgHis 284

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Sequence 15, Application US/09485077A

Sequence 15, Application US/09485077A

Sequence 15, Application US/09485077A

Sequence 15, Application US/09485077A

Sequence 15, Application

Sequence 15, Application

Sequence 15, Application

Sequence 15, Application

TITLE OF INVENTION: Methods and Compositions for Treatment of Restenosis

TITLE OF INVENTION: Methods and Compositions for Treatment of Restenosis

FILE REFERENCE NIH-05047

CURRENT FILING DATE: 2000-06-23

PRIOR PELING DATE: 1998-07-08

PRIOR FILING DATE: 1998-07-08

PRIOR FILING DATE: 1997-07-08

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Version 3.0

SEQ ID NO 15.
                                                                                                             3235 GCCACACCATCATCAAGATCTGATTCACAAGAGTCAAATACAAATGCATATAAAAACAAAT 3294
                               276 PheHisLeuSerSerArgArgArgHisGlnGlySer-----MetGlyTyrHisGlyAsp 293
                                                                                          294 MetTyrIleGlyAsnAspAsnGluArgAsnSerTyrGlnGlyHisPheGlnThrArgAsp 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValLeuGlyPheIleGlyLeuGlyLeuValValAlaIleLeuAlaLeuThrIleTrpGln 60
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Matches:
Conservative:
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Best Local Similarity:
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US-09-485-077A-15
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                                                              2755 GCGTCTGAAATGCATGTAGACGCTCCTAAAACGCAAGAGTACGCAGTAACTGAATCTCAA 2814
                                                                                                                                                                                                  314 GACTTAACAGATAATAGTACAGATGCTAGTCAGCTTCATACAAATGGCATAGAGAATGAA 2373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 ThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAsp----- 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 AlaSerAsnAspAspAsnValPheAspAspPheThrSerTyrAsnAlaHisLysLysLys 205
                                                                                                                                                                                                                                                                                                ---PheAspGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                          ------AspAspAspAspGlyAspGlyLeuAspSer-----Ile 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspValGlyAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHis 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SerProAlaProLeuHis----- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------HisArgArgArgMetHisSerArgHisArgHisLeuLeuValArg--- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- LysAlaArgSerGluAspSerArgProAlaAlaHis 275
                                                                                                                                      GAAATGTATGCTAAACAAGGGAACGCTATGTTGGTGATAGTTCATTAAATGATGATAGT
                                            GinThrThrArgValSerHisLeuAspLysGluLeuLysSerLeuLysArgValValAsp
                                                                                                                                                                                                                                                                2374 ACTGTATCAAATGATGAAAAAAAAAGCGTCAATACAAAATGAAGACACTAATGACACT
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                                                                                                       AsnLeuGlnGlnArgLeuGlyIleAsnTyrLeu----
             US-09-813-329-6 (1-409) x US-08-956-171E-39 (1-4522)
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US-09-813-329-6 (1-409) x US-09-206-576-1 (1-1424)
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                                         GAAGAAACCAATGACTTTAAACAAGAG---
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523 GTAGAC---ACATATGATGACCCAAGGTGATGTGGTTTATGGACTGAGGTCAAAATCT 579
                                                                                                                                                580 AAGAAGTITCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAGGACATCACCTCA 639
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                                                                                                                                                                                                                                                             AspPheThrSerTyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSerIleAla 214
                                                                                                                                                                                                                                                                                    GAC---CAGAGTGCTGAAACCCACAGAGCAGTCCAGATTATATAAAGCGGAAAGCC 816
                                                                                                                                                                                                                                                                                                        215 AspValArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSer 234
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------ANTGATGAGAGCAAT-----GAGCATTCCGATGTGATAGTCAG 858
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                                                                                                                                                                                                                                                                                                                                                                                                                  403 GACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGATGAATCTG
                                                      463 GTCACTGATTTTCCCACGGACCTGCCAGCAACCTTTTCACTCCAGTTGTCCCCACA
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Parent No. 6551990

GENERAL INFORMATION:
APPLICANT: Giachelli, Cecilia M.
APPLICANT: Steitz, Susie
TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification
FILE REFERENCE: P-UW 3244
CURRENT APPLICATION NUMBER: US/09/206,576
CURRENT FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SSEQ ID NO 1
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Matches:
Conservative:
Mismatches:
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Gaps:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-09-206-576-1
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| CACCAGTCTGATGAGTCTGATGAATCTGATGAACTGGTCACTGATTTTCCC 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                AsnLysLeu----AsnAsnAlaHisThrGlyThrThrProThrSerGluThrThrAla 174
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                                                                                                                                         TCCAACGAAAGCCATGACCACATGGATGATGGATGATGATGATGATGATGATGATGTGTGTGTG
AspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLys
                                                        --ACCCTTCCAAGTAAG
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536 GATGGCCGAGGTGATGGTTTATGGACTGAGGTCAAAATCTAAGAAGTTTCGCAGA
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Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

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Scoring table:

US-09-813-329-6

Perfect acore: Sequence:

seg length: 0 seg length: 200000000

Minimum DB e Maximum DB e

Database :

Total number

Searched:

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Sequence 5, Application US/09813329
Patent No. US20020012968A1
Patent No. US20020012968A1
Patent No. US20020012968A1
Patent No. US20020012968A1
TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class MolecTITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
REACH APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
                                                                                                                              Sequence 447, App Sequence 52112, A Sequence 5112, A Sequence 14, Appl Sequence 1, Appl Sequence 1, Appl Sequence 6, Appl Sequence 6, Appl Sequence 41, Appl Sequence 6, Appl Sequence 24791, A Sequence 19, Appl 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2682, Ap
Sequence 16858, A
Sequence 16858, A
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Sequence 271, Appl
Sequence 19, Appl
Sequence 1, Appli
Sequence 107179,
Sequence 87071,
Sequence 69258, A
Sequence 6017, A
Sequence 58, Appl
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Sequence 61685, A
Sequence 6421, Ap
Sequence 8857, Ap
Sequence 6025, Ap
Sequence 4557, Ap
Sequence 25862, Ap
                                                                               Sequence 45792, A
Sequence 46034, A
Sequence 447, App
Sequence 52112, A
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3 US-10-437-963-45792

3 US-10-437-963-52112

3 US-10-425-114-734

0 US-09-729-658B-14

1 US-10-728-411-6

5 US-10-728-411-6

5 US-10-728-328A-6

5 US-10-728-328A-6

5 US-10-218-328A-6

5 US-10-218-328A-6

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1 US-10-437-963-6017

1 US-10-437-963-6018

1 US-10-437-963-61885

1 US-10-329-624-39

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1 US-10-329-624-39
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3 US-10-0425-114-4557

105-09-938-842A-2682

1 US-09-938-842A-2682

3 US-10-425-114-16858

3 US-10-425-114-16858

5 US-10-047-963-95865

5 US-10-047-963-95865

5 US-10-097-349-13

5 US-10-097-340-230

5 US-10-097-341-175
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; NAME/KEY: CDS
; LOCATION: (634)..(1860)
US-09-813-329-5
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-MODEL=frame+ pan.model -DEV=xlp
-MODEL=frame+ pan.model -DEV=xlp
-G-Cgn2 1/USFTC spool p/US09931329/runat_13092004_102755_21784/app_query.fasta_1.583
-G-Cgn2 1/USFTC spool p/US09931329/runat_13092004_102755_21784/app_query.fasta_1.583
-DB-Published Applications NA -OFMT=fastap -SUFFTX=rnpb -MATRIX=blosum62
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR MAXCEN=EPCT -THR MAXLEN
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09813329_@CGN i 1 912_@runat_13092004_102755_21784
-NCPUS=C -ICPUS=3 -NO MANAP -LARGEQUERY NEG SCORES=0 -MATT -DSBELOCK=100
-LONGLOG -DEV TIMEOUT=30 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5
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2765.985 Million cell updates/sec
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                                                                                                                                                               September 15, 2004, 10:23:37; Search time 744 Seconds
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                          nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Query Match Length DB

Score

Result

Pred. No. is the number of

Db 1534 GAGAGAAACTCTTATCAGGGACACTTTCAAACGCGCGATGGCGTCACTTGACGGTGACCAAT 1593	Db 1714	RESULT 2 US-09-0813-329-3 1 Sequence 3, Application US/09813329 1 Sequence 3, Application US/09813329 1 Sequence 3, Application US/09813329 1 Factor No. US2002012968A1 1 GENERAL INFORMATION: 1 TITLE OF INVENTION: No. US20020012568A1e1 Drosophila Tumor Necrosis Factor Class 1 TITLE OF INVENTION: Natiants Thereof 1 FILE REFERENCE: D0016.np 1 CURRENT APPLICATION NUMBER: US/09/813,329 1 CURRENT FILING DATE: 2001-03-20 1 PRIOR APPLICATION NUMBER: 60/190,816 1 PRIOR APPLICATION UNMBER: 60/190,816 1 NUMBER OF SEQ ID NOS: 65	2 4 9 0 7 8 9 5	US-09-813-329-6 (1-409) x US-09-813-329-3 (1-1221) QY
Alignment Scores: Pred. No.: 1.088-233 Length: 2148 Score: Score: Percent Similarity: 100.00\$ Matches: 409 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Mismatches: 0 Best Local Similarity: 100.00\$ Mismatches: 0 US-09-813-329-6 (1-409) x US-09-813-329-5 (1-2148) Qy 1 MetThxAlaGluThrLeuLySProPhelleThrProThrSerAlaAsnAsbAspGlvPhe 20	634 ATGACTGCGGAGACCCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGTTTTTTTT	ThrThrArgValSerHisLeuAspLysGluLeuLysSerLeuLysArgValValAspAsn 80	Db 994 GACGATGGCGATGGTTCATTCATTCATACGGACGACGATGTTTTTTTT	

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Sequence 1, Application US/09813329
Patent No. US20020012968A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Suibb Company

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INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class
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TITLE OF INVENTION: No. US20020012968A1el Dr
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
FRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                        TYPE: DNA
ORGANISM: Drosophila melanogastor
                                                                                                                                                                                                                                       1.84e-220
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96.82%
96.33%
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US-09-813-329-1
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Best Local Similarity:
Query Match:
DB:
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NAME/KEY: CDS
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Pred. No.:
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Sequence 46034, Application US/10424599
Sequence 46034, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Can Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 46034
LENGTH: 1269
                                                                                         1411 CTCACCTACTTCGAGTACCGCCGCGCTCAAGAGA---GAGAAGCTCCGCAAGAGCATGAAG 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      829 TTGAGGGACAGTAAGAAGAAGAGCCGGAGCTCAĆĠGAGGAAGAGGAAGCAAGCAGTCTGAT 770
                                                                                                                                76 ArgValValAspAsnLeu-----GlnGlnArgLeuGly------Ile 87
                                                         LeuThrlleTrpGlnThrThrArgValSerHisLeuAspLysGluLeuLysSerLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 AsnAlaHisLysLysGlnGluArgLysSerArgSerIleAlaAspValArgAsnGlu
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                                                                                                                                                                                                                                                                                                                                                                   1192 GAATCCGACTCCGGTGATCTGATAGCTTGTCCGATTCCAGCAAATCAGAT-----
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; Beduence 45792, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Brabazuk, Brad
; APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21/3221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NO AFFO. IN OUR SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                            AAAGAGAGCCTGCAGCACTTCACCTCCGTCGCAGAATGCATTCCCGCCATCGCCACCTC 1431
                                                                                                                                                            GTAGTCCGCAAAGCCAGATCCGAGGACTCGAGGCCAGCAGCCCATTTCCACTTGAGCAGC 1491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgArgArgHisGlnGlySerMetGlyTyrHisGlyAspMetTyrIleGlyAsnAspAsn 300
                                                       LysGluSerProAlaProLeuHisHisArgArgArgMetHisSerArgHisArgHisLeu 260
                                                                                                                                                                                                                                                                                                                                             ThrGlyLeuTyrTyrValTyrAlaGlnIleCysTyrAsnAsnAsnSerHisAspGlnAsnGly 340
                                                                                                                                                                                                                                                                                                                                                                                                                PhellevalPheGlnGlyAspThrProPheLeuGlnCysLeuAsnThrValProThrAsn 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetProHisLysValHisThrCysHisThrSerGlyLeuIleHisLeuGluArgAsnGlu 380
CAGAATATTCAAGGAAATCACACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAGCTTCC
                                                                                                                            LeuValArgLysAlaArgSerGluAspSerArgProAlaAlaHisPheHisLeuSerSer
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US-10-437-963-45792
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ORGANISM: Oryza sativa
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Best Local Similarity:
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ORGANISM: Candida albicans
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 ThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAspSerAla 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 GlnGlyAsnHisThrGluLeu-GlnGluLysSerSerAsnGluAlaThrSerLysGluSe 243
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                                                                                                                                                                                                                                                                                             184 SerSerAlaSerAsnAspAspAsnValPheAspAspPheThrSerTyrAsnAlaHisLys 203
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                                                                                                                                                                           AsnAspAspGlyPheProAlaLysAlaThrSerThrAlaThrAlaGlnArgArgThrArg
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Matches:
Conservative:
Mismatches:
Indels:
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           ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14156C.1
US-10-424-599-46034
                                                                             143.00
35.69%
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Best Local Similarity:
Query Match:
ORGANISM: Glycine
                                                        Alignment Scores:
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Sequence 447, Application US/10451467A

Sequence 447, Application US/10451467A

Publication No. US20040161840A1

Seberation No. US20040161840A1

Septicant: CONTRERAS, ROLAND HENRI

APPLICANT: EBERHARDY, INES

APPLICANT: REBERANGS, EIREA JOSEPHINA

TITLE OF INVENTION: YEAST AND FUNG!

FILE REPERBRENCE: JAB-1667

CURRENT APPLICATION NUMBER: EP 00870318.3

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR PAPLICATION NUMBER: EP 01870002.1

PRIOR PLING DATE: 2001-01-04

PRIOR PLING DATE: 2001-01-04

PRIOR PLING DATE: 2001-01-09

NUMBER OF SEQ ID NOS: 732

SEQ ID NO 447

TUDE OF INVENTION OF SEQ ID NOS: 732

SEQ ID NO 447

TUDE OF INVENTION OF SEQ ID NOS: 732

SEQ ID NO 447

TUDE OF INVENTION OF SEQ ID NOS: 732

SEQ ID NO 447
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                                                280 rArgargaighisGlnGlySerMetGlyTyrHisGlyAspMetTyrIleGlyAsnAspAs 300
                                                                         ThraspGluGluaspaspaspaspGlyaspGlyLeuaspSerIleAlaaspaspGluasp 134
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326 GGCGAGGAGGAGGAAGAAGATGTCGATGATGATGGTGAGAAGTCTGAGGCTCCACCA 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 TTAGCAGGCAAAGAATTACCAAAAGTTTCTAAACAGTTGGAATCCATTATTGATGAAGTG 375
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Should R
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: | | | :: 11045 GGAACATGGGTCACCGGCGGCCTAGGTGGCCAAGCAATCTTCCTCAGTGAACTC 1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                   117 GluGluAspAspAspAspGlyAspGlyAspGlyLeu-----AspSerIleAlaAspAspGluAsp 134
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Mismatches:
Indels:
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ORGANISM: Glycine max
; FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_44746C.1
US-10-424-599-81649
    ; ORGANISM: Oryza Bativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5443C.1
US-10-437-963-52112
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Matches:
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                                                                                                                       1.43e-05
140.50
42.358
25.88%
6.50%
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Buchharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANTON: Blants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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1153 GGAGAAAAGGCTAGTGAAAAATTATTACAAGTCAGAGGTAAAGATTTCACAAAGAATAAA 1212
ThralaGluGlyGluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnVal 192
                                                                                                                                                                                      676 AGTTCCGACTCAAAATCTGAACTCAGACTCAAGCTCCAGCTCTGATTCAAGTTCT 735
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                                                                 154 AspMetLeuAsn---LysLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThr 172
                                                                                                                                                                                                                                                                                                                                                                      226 AsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThrSerLysGluSerProAla 245
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                                                                                             1213 AATAAAATGAAGAGGAAGTTATAAAGGA
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: AVOVALIC, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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LENGTH: 1221
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                       67 LeuAspLysGluLeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeuGly
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                  ; OTHER INFORMATION: Clone ID: 700727423_FLI
US-10-425-114-7734
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7734
LENGTH: 966
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Best Local Similarity;
Query Match:
DB:
                                                                                       TYPE: DNA
ORGANISM: Glycine
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Pred. No.:
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Sequence 1, Application US/09729658B;
Sequence 1, Application US/09729658B;
Publication No. US2003002391A1
GENERAL INFORMATION:
APPLICANT: Zonana et al.
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 55924 WOOP/120, 658B
CURRENT APPLICATION NUMBER: US/09/729, 658B
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/12-04
PRIOR APPLICATION NUMBER: 60/12,366
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
SEQ ID NO 1
TYPE: DNA
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                                   683 CCCCTGGCCTCCAGGGACCTTCTGGTGCTGCTGATAAAGCTGGAACTCGAGAAAACCAGC 742
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                                                                                                       ----ValArgAsnGluGluGlnBsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSe
----LysSerArgSerIleAlaAsp--
                                                                                                                                       sSerArgHisArg---HisLeuLeuValArgLysAlaArgSerGluAspSer-----
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ORGANISM: Homo sapiens
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LOCATION: (1)
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US-09-729-658B-14
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	Db 1032 ATGATCTTTCAGGTGGAGTGCTCAATGACTCGCATCACTATGAACCCCAAGGTGT 1091 Qy 307 lyHisPheGlnThrArgAspGlyValLeuThrValThrAsnThrGlyLeuTyrTyrValT 327 Db 1092 TTAAGCTACATCCCCGCAGCGGAGCTGGAGGTACTGGACGGCACCTACTTCATCT 1151 Qy 327 yrAlaGlnIleCysTyrAsnSerHisAspGlnAsnGlyPheIleValPheG 345	Db 1152 ÄTAGTCÄĞGTAGAAGTATACTÄĆATCÄÄCTTCACTGÄCTTTGCCAGGTATGAGĞTGG 1211 Qy 345 lnGlyAspThrProPheLeuGlnCysLeuAsnThrValProThrAsnMetProHisLysV 365	1212 TGGATGAGAAGCCCTTCCTGCAGTGCACACGCAGCATCGAGACGGGCAAGACCAACT	Qy 365 alHisThrCysHisThrSerGlyLeuIleHisLeuGluArgAsnGluArgIleHisLeuL 385	Oy 385 ysAspIleHisAsnAspArgAsnAlaValLeuArgGluGlyAsnAsnArgSerTyrPheG 405	Qy 405 lyllePheLyBVal 409	RESULT 12 US-10-202-062-41 ; Sequence 41, Application US/10202062 ; Publication No. US20040038349A1	; GENERAL INFORMATION: ; APPLICANT: Human Genome Sciences, Inc., ; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members ; FILE REPERENCE: PF559	CURRENT APPLICATION NUMBER: US/10/202,062 CURRENT FILING DATE: 2002-07-25 FILING DATE: 20/307,838	FILMS TAILED FALLS (LILLING DAEL : 2011-27) FUNDRER OF SEQ ID NOS: 42 SOFTWARE: PatentIn version 3.0 FLENGTH: 5307	TYPE: DNA CORCANISM: human FEATURE: NAME/KFY: misc feature	; LOCATION: (4242);(4242); OTHER INFORMATION: n equals a, g, c or t; FEATURE; PEATURE; nisc feature	; LOCATION: (4471); (4471); (7THEN INFORMATION: n equals a, g, c or t; FATURE; FATURE; NAME/KEY: misc feature		; LOCATION: (4523)(4523) ; OTHER INFORMATION: n equals a, g, c or t ; FEATURE:	; NAME/ABI MIBC FEBRUIE ; LOCATION: (4529) ; COMMER INFORMATION: n equals a, g, c or t	; NAME/KEY: misc feature ; LOCATION: (4531)(4531) ; OTHER INFORMATION: n equals a, g, c or t
) ORGANISM: Homo sapiens) FEATURE:) NAME/KEY: CDS US-09-729-658B-1	Alignment Scores: Pred. No.: Score: 138.00 Matches: Percent Similarity: Best Local Similarity: 10 Guery Match: 10 Gaps: Predict Score: 137.4 Matches: 157 Mismatches: 167 Mismatches: 177 Mismatches: 187 Mismatches: Mi	-09-813-329-6 (1-409) x US-09-729-658B-1 (1-1574)	Oy 35 ArgGlnLeuIlePro-LeuValLeuGlyPheIleGlyLeuGlyLeuValValAlaIleLe 54	Qy 54 uAlaLeuThrIleTrpGlnThrThrArgValSerHisLeuAspLysGluLeuLysSerLe 74	74 uLysargValValAspasnLeuGlnGlnArgLeuGlyIleAsnTyrLeuAspGluPheAs 442 GTTGCGGCGGAACGTGGAACGACGACTGACTTGACTAGACTAGACTAGACTAGATTGAACTAGATTGAACTAGATTGAACTAGATTGAACTAGATTGAACTAGATTGAACTAGATTGAACTAGATTGAACTAGATTGA	94 pGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGlyLe	Qy 114 uThrAspGluAspAspAspAspAspGlyAspGly	Qy 127 pSerIleAlaAspAspGluAspAspAspAspAslSerTyrSerSerValAspAspValGl 146	LeuAsnAsnAlaHisThrGly 1	166 -ThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluTh 116 -ThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluTh 11	BnAl:	ap	yase - ccrc	-H 4	Oy 254 sSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAspSer 270	271	Db 924 CCCCTGGCCTCCAGGGACCTTCTGGTGCTGCTGATAAAGCTGGAAACTCGAGAAAACCAGC 983 Qy 273 a-AlaHisPheHisLeuSerSerArgArgArgHisGlnGlySerMetGlyTyrHisG 292

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                                                                                                               307 lyHisPheGlnThrArgAspGlyValLeuThrValThrAsnThrGlyLeuTyrTyrValT
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; Sequence 6, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
    APPLICANT: Barnes Jewish Hospital
; APPLICANT: Law, Jonathan
; APPLICANT: Law, Conathan
; APPLICANT: Leichbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO

LEMENTH: 5307
                                                                            292 lyAspMetTyrIleGly-----AsnAspAsnGluArg
     985 CAGCTGTGGTGCATCTACAGGGC----
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LOCATION: (4531)...(4531)
OTHER INFORMATION: n = a, t, c
FEATURE:
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LOCATION: (4471)...(4471)
OTHER INFORMATION: n = a,
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NAME/KEY: misc feature
LOCATION: (4242). (4242)
OTHER INFORMATION: n = a
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OTHER INFORMATION: n = a
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OTHER INFORMATION: n = a
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LOCATION: (4529)..(452)
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     ; FEATURE:
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; LOCATION: (4545)..(4545)
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Matches:
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Indels:
NAME/KEY: misc_feature
LOCATION: (4545)..(4545)
OTHER INFORMATION: n = a, t, c or g
OTHER LOCATION: IN = a, t, c or g
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/NM_001399.1
DATABASE ENTRY DATE: 2000-10-31
RELEVANT RESIDUES: (1)..(5307)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1998-11-13
RELEVANT RESIDUES: (1)..(5307)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/AF061189.1
DATABASE ACCESSION NUMBER: NCBI/AF061189.1
DATABASE ENTRY DATE: 1998-11-14
RELEVANT RESIDUES: (1)..(5307)
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel.
TITLE OF INVENTION: Human Endokine Alpha
FILE REPERENCE: PF61
CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR PILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.1
SEQ ID NO 41
LENGTH: 5307
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FEATURE:
NAME/KEY: misc_feature
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LOCATION: (4242)..(4242)
OTHER INFORMATION: n equals
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LOCATION: (4471)..(447)
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                                        sSerArgHisArg---HisLeuLeuValArgLysAlaArgSerGluAspSer-----
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Publication No. US20030109444A1
GENERAL INFORMATION
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Partick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0206
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CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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OTHER INFORMATION: n = a,
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NAME/KEY: misc feature

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OTHER INFORMATION: n = a, t,

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NAME/KEY: misc feature

LOCATION: (4531)..(4531)

OTHER INFORMATION: n = a, t,

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NAME/KEY: misc feature

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COCATION: (4545)..(4545)

OTHER INFORMATION: n = a, t,

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1033 ATGATCTTTCAGGTGGAGTGCTCAATGACTGGTCTCGCATCACTATGAACCCCAAGGTGT 1092
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                                                                                                                                                                                                                                                                                             292 lyAspMetTyrIleGly-----AsnAspAsnGluArg-----AsnSerTyrGlnG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 lnGlyAspThrProPheLeuGlnCysLeuAsnThrValProThrAsnMetProHisLysV 365
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254 sSerArgHisArg---HisLeuLeuValArgLysAlaArgSerGluAspSer----- 270
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                                              865 TTCCAGGAACAACTGTTATGGGACCACCTGGTCCTCCAGGTCCTCGTGGTCCTCAAGGAC
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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- nucleic search, using frame plus p2n model
OM protein
                                    Run on:
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(without alignments) 2914.948 Million cell updates/sec US-09-813-329-6 2162 1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409 September 15, 2004, 05:12:07; Search time 4190 Seconds 0.0 0.0 0.0 Xgapop 10.0 , Xgapext (Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Title: Perfect score: Sequence: Scoring table:

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55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	94 BG636194 SD13795.5	BI636564	CK135985	CK135525	BX560278	BX553466	A1253821 /	ALL 105396	BII77518	CF590046	CD851068	BI514804	BU798281	BU803616	AY223179	CD509148	BC049115 Mus	BA62058U BA62	BCC20333 Mus	BC023777 Mus	AY401339 Mus	BU445245	BU911456 AGEN	BX560279	BX269011	BI250058	BC03364	BLICTON STATE	BU117025	BX026465	BF482404	BI249241	BI250570	CA473339	BI250061	BU771970 S.	CA855938 PI	BU149401 AC	BJ379142 BC	BM203188	BJ617087 BC
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ALIGNMENTS

RESULT 1

BG656194 linear EST 23-APR-2001 SD13795.Sprime SD Drosophila melanogaster Schneider L2 cell culture DCT2 Drosophila melanogaster CDNA clone SD13795 5 similar to CG12919: PBan0012919 located on: 2R 46E1-46E1;: 04/13/2001, mRNA Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, BG636194 BG636194.1 GI:13763731 Drosophila Drosophila seguence. EST. BG636194 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

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SD18286.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD18286 S similar to CG12919: FBan0012919 GO:[] located on: 2R 46El-46El;: 05/19/2001, BI636564.1 GI:15538774
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                                                                                                                                                                                                                                                                                  Tr. (bases i to 495)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Harvey, D., and Rublin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46E4: 05.19/2001
Plate: SD.182 row: H column: 2
High quality sequence stop: 491.
Location/Qualifiers
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                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
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Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 686)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Ebdis, S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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                                                                                                                                                              Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AB003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46B4: 04/13/2001
Plate: SD.137 row: H column: 11
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Location/Qualifiers
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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

TITLE

COMMENT

REFERENCE AUTHORS

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Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: $10 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003831 arm:2R [4876906,5137815]
estimated-cyto:46813-46E4: 08/05/2002
Plate: RH.516 row: E column: 11
High quality sequence stope: 382.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CK135525
RHS169.3prime RH Drosophila melanogaster normalized Head pFIC-1
Drosophila melanogaster TONA clone RHS1659 3 similar to CG12919:
FBan0012919 GO:[] located on: 2R 46E1-46E1; 08/05/2002, mRNA
                                                                                                                           364 LysValHisThrCysHisThrSerGlyLeuIleHisLeuGluArgAsnGluArgIleHis 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopera; Badopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 532)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
Misra, S., Mungall, C.J., Nunoo, J., Parlso, J., Paragas, V., Park, S.,
Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
                          508 TATTACGTATACGCCCAGATATGCTACAACAACTCGCACGACCAGAACGGATTATCGTC 449
                                                                                                                                                                                                                                                                                                                                                 344 PheGlnGlyAspThrProPheLeuGlnCysLeuAsnThrValProThrAsnMetProHis 363
                                                                                                                                                                                                                                                                                                       384 LeuLysAspIleHisAsnAspArgAsnAlaValLeuArgGluGlyAsnAsnArgSerTyr 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mkNA"
/db_xref="taxon:7227"
/clone="RH1659"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
/clone_lib="RH Drosophila melanogaster normalized Head
                                                                                                                                                                                                                                  388 AAGGIGCACACCTGCCACACGAGTGTGTGATCCACCTGGAAACGAAAACGAGAGGATCCAT
324 TyrTyrValTyrAlaGlnIleCysTyrAsnAsnSerHisAspGlnAsnGlyPheIleVal
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Other_ESTs: RH51659.5prime
                                                                                                                                                                                                                                                                                                                                                                                                         404 PheGlyIlePheLysVal 409
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CKI35525.1 GI:38627461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003831: arm:2R [4876906,5137815]
estimated-cytc:46B13-46E4: 02/08/2002
Plate: SD.182 row. H column: 2
Plate: SD.182 row. H column: 2
High quality sequence stoop: 456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CK135985 508 bp mRNA linear EST 02-DEC-2003 SD18286.3prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster CDNA clone SD18286 3, mRNA sequence.
                                                    305 AATGCCCACAAAAAGAAGCAGGAGAGAAATCTCGCTCGATTGCCGATGTGCGCAATGAG 364
                                                                                                                                                   365 GAGCAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACT 124
                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota: Metazoda; Arthropoda; Haxapoda; Insecta; Pterygota;
Eukaryota: Metazoda; Arthropoda; Haxapoda; Insecta; Pterygota;
Noppera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

(Dases 1 to 508)
Harvey, D., Brokatein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Other ESTs: SD18286. Sprime
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/clone_lib="SD Drosophila melanogaster Schneider L2 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pOT2; Site 1: EcoRI; Site 2: Xho1; Sized fractionated cDNAB were directly ligated into pOT2. Plasmid cDNA library."
                       AsnAlaHisLysLysLysGlnGluArgLysSerArgSerIleAlaAspValArgAsnGlu
                                                                                                                      GluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThr
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/db_xref="taxon:7227"
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FEATURES

Pred. No.:

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Mismatches:
Indels:
Gaps:
                                                                                       Length:
Matches:
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Genome Biol. 4 (10), R63 (2003)
                                                                                                                                                                                     (1-612)
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Glossina morsitans morsitans
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BX553466.1 GI:33377624
                                                                                  2.99e-25
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Best Local Similarity:
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                                                                        Alignment Scores:
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BX553466
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at 5'
end of the CDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX560278 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse49al0_plc, mRNA sequence.
                                                                                                                                                                                                                                                                                                             530 TACGTATACGCCCAGATATGCTACAACAACTCGCACGACCAGAACGGATTTATCGTCTTT 471
                                                                                                                                                                                              GlnGlyAspThrProPheLeuGlnCysLeuAsnThrValProThrAsnMetProHisLys 364
                                                                                                                                                                                                                470 CAAGGAGACACTCCATTCTTGCAGTGCTTGAACACGGTGCCCACCAACATCCCACCATAAG 411
                                                                                                                                                                                                                                                    ValHisThrCysHisThrSerGlyLeuIleHisLeuGluArgAsnGluArgIleHisLeu 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                         Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans and expression analysis of putative immune
                                                                                                                                         TyrValTyrAlaGlnIleCysTyrAsnAsnSerHisAspGlnAsnGlyPheIleValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Glossina morsitans morsitans"
             532
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Matches:
Conservative:
Mismatches:
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/sub_species="morsitans"
/db_xref="taxon:37546"
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Genome Biol. 4 (10), R63 (2003)
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BX560278.1 GI:33368472
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466.00
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Alignment Scores:
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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 AspGlyValLeuThrValThrAsnThrGlyLeuTyrTyrValTyrAlaGlnIleCysTyr 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 AsnAsnSerHisAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGln 352
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1 (Dases 1 to 539)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
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/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 IGCTTTCAAACTGTACCACTAACATGTCACTGAAAATCCACACTTGTCATACGAGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 AlaValLeuArgGluGlyAsnAsnAsnArgSerTyrPheGlyIlePheLyBVal 409
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Thinxton, Cambridge, CB10 18A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
Bangor LL57 2UW
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/tissue_type="Byestalk"
/dev_stage="Mature broodstock"
/clone_lb="Giant tiger prawn eyestalk cDNA library"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
Xho!; mRNA isolated from total eyestalk tissue and used to
construct directional cDNA library in Lambda ZAP Express.
Clones excised in vivo to create phagemids in pBK-CWV for
                                                                         Tiger Shrimp
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 Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                              Tel: +61 7 4753 4444

Fax: +61 7 4775 5852

Fax: +61 7 4772 5852

No significant database matches when searched using a filter to remove low-complexity sequence, September 3 1998. When searched with the filter turned off, shows homology to large proline-rich protein bat2 from humans (p= 2.0e-07)

Insert Length: 1000 Std Error: 100.00
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Townsville QLD 4810, Australia
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Matches:
Conservative:
Mismatches:
Indels:
                                                     Lehnert, S.A., Wilson, K.J., Byrne, K. and
Tissue-Specific Expressed Sequence Tags
                                                                                          Penaeus monodon
Mar. Biotechnol. 1 (5), 465-476 (1999)
Contact: Wilson Kate J
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Penaeus monodon"
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                                                                                                                                                               Australian Institute of Marine PMB 3, Townsville Mail Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bequencing."
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193.50
46.96%
32.60%
8.95%
                                                                                                                                                Marine Biotechnology
                     Penaeidae; Penaeus.
1 (bases 1 to 526)
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AUTHORS
TITLE
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                                                                                                                                \bar{l} note="country: Zimbabwe; EST from adult gut infected with T.bruce1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCTGGCATTTAATACTTATAACGAATTTAAGACTCGCTAACGAAAATAATACGCACAGT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTAGAGATCTTCAAAAGGAAGTCATTACACTCAACAAGATCATTGAAAGTCTACAGAAA 168
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                                                  /db_xref="taxon:37546"
/clone="Tsel29f05 glc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGGCAATTGTTTTGACTTTTGTA---------CTCTTGGGTTGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                          38 IleProLeuValLeuGlyPheIleGlyLeuGlyLeuValValAlaIleLeuAlaLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleTrp------GlnThrThrArg
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organism="Glossina morsitans morsitans"
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Matches:
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Mismatches:
Indels:
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Penaeus monodon
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206.50
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Library Submitted (108-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: 1057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzil; Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta. Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                           Candida tropicalis
Candida tropicalis
Candida tropicalis
Candida tropicalis
Candida tropicalis
Edwaryota; Fungi; Ascomycota; Saccharomycetales; Candida.
Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 917)
S Soucit. J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

1 (564711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 917)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
                                                                                                                                   CNSO7DXT
T3 end of clone BD0AA016E09 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <10. .>383
/note="similar to Saccharomyces cerevisiae ORF YKL088w
similarity to C.tropicalis hal3 protein, to C-term. of
Sis2p and to hypothetical protein YOR054c |
1 putative frameshift(s)"
/evidence=not_experimental
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 487 (1), 91-94 (2000)
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AL441063.1 GI:12224469
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                                                 436 GAT 438
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                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence T7 end of BACN37D20 of DrosBAC library from Drosophila melanogaster (fruit AL10), genomic survey sequence.
AL108596. I GI:5628900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaser BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                               CACCGGGGGCCCACCTACCTTCCCAGGAACGCTGCCGTCTACATCCGGGACCTGGACCA 458
                                                                                                                             PheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGlyLeuThr 115
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sThrSerGlyLeuIleHisLeuGluArgAsnGluArgIleHisLeuLysAspIleHisAs 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 TIGCAGAWMIGGCAGAMAAMRCGIGIAITCGCAICTIGGACAAAGAACTIGAAAAACCIGAAV 315
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                                                                                                 389 nAspArgAsnAlaValLeuArgGluGlyAsnAsnArgSerTyrPheGlyIlePheLysVa
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone="BACN37D20"
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/plasmid="pBeloBAC11"
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                                                                                                                                      /mol_type="mRNA"
/strain="Compton Line 151"
                                                                                                                      organism="Gallus gallus"
                              PO Box 88, Manchester, M60 10D, U
121: 01612208930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                   /db_xref="taxon:9031"
/clone="ChEST800c8"
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                                                                                           Location/Qualifiers
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/lab_host="DH10B"
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Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                      338
                                                                                                                                                                                     396 AGGTTATTAGATGAA---GAAGAAGATTG-----AATGAAGAGGACGAAGAAGATGAG 446
                                                                                                                                                                                                                                                                                         PheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGlyLeuThr 115
                                                                                                                                                                                                                                                                                                                      447 GATGAAGAAGAGGGTGATGACGGC------GAAGAAGAIGGTGATGCG 488
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                                                                                                                                                                                                                               ArgValValAspAsnLeuGlnGlnArgLeuGlyIleAsnTyrLeuAspGluPheAspGlu 95
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                      40 LeuvalLeuGlyPheileGlyLeuGlyLeuvalValAlaIleLeuAlaLeuThrIleTrp
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Contact: Simon Hubbard
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/doce="Cran. kidney + adrenal; Vector: pBluescript II
//note="Crgan: kidney + adrenal; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: Not1; This normalized
library was constructed from 1 million independent clones.
CDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Not1 adapters, digested with
EcoRI; size-selected, and cloned into the Not1 and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CD851068 746 bp mRNA linear EST 11-JUL-2003 DH0AL5ZH01ZM1 HaDevR5 Helianthus annuus CDNA clone HaDevR55H01,
       348
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                                                                                                                                                                                                                                                                                                                                                 408
                                                                                                                                                                                                                                                                                                                                                                                                                  319 rAsnThrGlyLeuTyrTyrValTyrAlaGlnIleCysTyrAsnAsnSerHisAspGlnAs 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468
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                                                                                                                                                                                                                                                                   301 -GluArgAsnSerTyrGlnGlyHis---PheGlnThrArgAspGlyValLeuThrValTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 nGlyPhelleValPheGln------GlyAspThrProPheLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nCysLeuAsnThrValProThrAsnMetProHisLysValHisThrCysHisThrSerGl
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'clone_lib="HabevR5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           746
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Helianthus annuus
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/clone="HaDevR55H01"
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/cultivar="psc8"
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CD851068.1 GI:32534884
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/clone lib="NICHD_XGC_SwblN"
/clone lib="NICHD_XGC_SwblN"
/clone lib="NICHD_XGC_SwblN"
/clone lib="VetCor: pExpress-1; Site_1: EcoRV; Site_2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHD XGC_Swbl). Library
was constructed by Open Biosystems (Huntsville, AL)."
                                                                                                                                               CF590046 965 bp mRNA linear EST 26-SEP-2003
AGENCOURT_15681475 NICHD_XGC_SwblN Silurana tropicalis cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contract: Daniela S. Gerhard, Ph.D.

Contract: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 RmlOAO7 Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Rob Granger, University of Virginia

CDNA Library Preparation: Open Biosystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAMIAT4 row: g column: 24

High quality sequence start: 23

High quality sequence stop: 511.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae, Silurana.
1 (bases 1 to 965)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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542 AGCAAGCACACTTTCTTTGGGGCCATCCGCCTA 577
                                                                                                                                                                                                                                                                                                                                                                    Silurana tropicalis (western clawed frog)
Silurana tropicalis
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Conservative:

    .965
    /organism="Silurana tropicalis"

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/db_xref="taxon:8364"
/clone="IMAGE:7020818"
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Schistosoma japonicum Schistosoma japonicum Schistosoma japonicum Schistosoma japonicum Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Suristosomatoidea; Schistosomatoidea; Schistosomatoidea; Schistosoma. 1 (bases 1 to 724)
Hu, W., Yan, Q., Shen, D.K., Liu, F., Zhu, Z.D., Song, H.D., Xu, X.R., Yan, Z.J., Rong, Y.P., Zeng, L.C., Wu, J., Zhang, X., Wang, J.J., Xu, X.N., Wang, S.Y., Fu, G., Zhang, X.L., Wang, Z.Q., Brindley, P.J., McManus, D.P., Xue, C.L., Feng, Z., Chen, Z. and Han, Z.G. Evolutionary and biomedical implications of a Schistosoma japonicum Complementary DNA resource Complementary DNA resource (complementary DNA resource)
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SJF2ACB08 SJF Schistosoma japonicum cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 LeuGlnCysLeuAsnThrValProThrAsnMetProHisLysValHisThrCysHisThr 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 SerGlyLeulleHisLeuGluArgAsnGluArgIleHisLeuLysAspIleHisAsnAsp 390
                                                                                                                                                                                                                                                                                                                                           /clouding libe Brain Normalized Library, BB16"
/note="Organ: brain, Vector: pT713-Pac; Site 1: EcoR1;
Site_2: Not1; The BB16 library was contributed by the Soares laboractory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 GCTCAAGIGACACTICTIAGAAAGGAAGACGIITITAGIITITCAAGGAGGCIAGCICACCG 292
                                                                                                                                                   European bees, predominantly
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53 TCCAACGATGGGAGTGTTACCATTTATGAACCAGGATTGTATTTAGTTTTATGCACAGATT
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                                                                                                                                                                                                                                                                        /tissue_type="brain"
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/lab_host="DH108"
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Matches:
Conservative:
Mismatches:
Indels:
primer: AGCGGATAACAATTTCACACAGGA
                                                                                                  organism="Apis mellifera"
                                                                                                                         /mol_type="mRNA"
/strain="mixed strains of
Seq primer: Accourtment High quality sequence stop: 550. Location/Qualifiers
                                                                                                                                                                                                                            /clone="BB160016A20A06"
                                                                                                                                                                                                  db_xref="taxon:7460"
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BB160016A20A06.5 Bee Brain Normalized Library, BB16 Apis mellifera
CDNA clone BB160016A20A06 5', mRNA sequence.
BI514804.1 GI:15365178
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Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Pardinae, J., Robertson, H.M., Soares, B. and Robinson, G.E.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                     GATGAAAGTGATGAAGAAATTGACGCCATATTGGAT------TCCACGAACCCT
                                                                                                                       114 LeuThraspGluGluaspaspaspaspaspGlyaspGlyLeuaspSerilealaaspaspGlu
                                                                                                                                                                     222 GCTCTGGATGCTGACGGTGATTATGATTACGATAATCTGGACGAAATCGCTGACGAC
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282 GATGATGATTGGTGGTAATGCTAGTGATGATGAAGGAATGGAGTTT-------
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Tel: 217 265 0309
Fax: 217 244 3499
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570 AAGAAGGCTAAAAAG 599
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Department of Entomology
University of Illinois
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Schistosoma japonicum
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                                                                                                                                                                                                                                                                                                                                                                                                                          91 AspGluPheAspGluPhe-----GlnLysGluTyrGluAsnAlaLeuIleAspTyr 107
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------AAGTTATCAAATGCACAA-----AATCTCGTATCTTCTCAAGTATCTACC 408
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          Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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52
                                                                                                                                       /organism="Schistosoma japonicum"
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/db_xref="taxon:6182"
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Mismatches:
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                                                                                                                                                                                              tissue type="Whole body"
/dev stage="adult"
/lab_host="rabbits"
/clone_lib="SJF"
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                                                                                              Email: hanzg@chgc.sh.cn.
Location/Qualifiers
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Hu, W., Yan, Q., Shen, D.K., Liu, F., Zhu, Z.D., Song, H.D., Xu, X.R., Wang, Z.J., Rong, Y.P., Zeng, L.C., Wu, J., Zhang, X., Wang, J.J.,
Xu, X.N., Wang, S.Y., Fu, G., Zhang, X.L., Wang, Z.Q., Brindley, P.J.,
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                                                                                                                                                                                                                                                                                   Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 AATAAAAATCTCGAAGTCGTAGTCCATCGTCTCTCCGGACTCAGATTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 GATGAATTTGATGAGTTCGGTCGTAAAAAAAAGTTATCGGCGAAGTCAAAGTGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 CTTAGTAACCATGACTCGTCCGATTCTGGTAACAATAATGCTACACCAGGACATGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrAspGluGluAspAspAspAspGlyAspGlyLeuAspSerIleAlaAspAspGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 AATGATGAAAATGTCAATAACAAAGGTAGTACAAGATGATGAAGATGAAGATTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 GluGlyGluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnValPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 TCATCATCCAGCCAGACTTCACATTCCTCACAATCAGATTCATCAAGTTCTCGTAGT
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                 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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/mol_type="mRNA"
/db_xref="taxon:6182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="Whole body"
/dev_stage="adult"
/lab_host="rabbits"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="SJF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="female"
Schistosoma japonicum
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143.00
43.26%
25.28%
6.61%
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188 GAGTCATCTTCCAAACCCGAAAAT---CAATCCAACGGCAAGAGACCTCATCCTAAAAAT 132

DEFINITION ACCESSION VERSION KEYWORDS

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